

OM nucleic - nucleic search, using sw model

Run on: May 5, 2004, 03:32:20 ; Search time 310.462 Seconds  
(without alignments)  
9578.440 Million cell updates/sec

Title: US-10-005-429-13

Perfect score: 700  
Sequence: 1 ggaacccacacgggaag.....aaaaaaaaaaaaaaaaaaaaa 700

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001as:\*  
5: Geneseq2001bs:\*  
6: Geneseq2002s:\*  
7: Geneseq2003as:\*  
8: Geneseq2003bs:\*  
9: Geneseq2003cs:\*  
10: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	188	26.9	540	9	ADC06863	Adc06863 Plasmid p
2	195.6	26.5	686	2	AAQ78205	Gene codi
3	185.6	26.5	687	3	AAQ6375	Rice thio
4	184.8	26.4	680	9	ADC08864	Plasmid p
5	172.8	24.7	659	9	ADC08860	Plasmid p
6	137.2	19.6	318	7	ABX87408	Corn ear-
7	120	17.1	382	3	AAQ62456	Wheat thi
8	119.6	17.1	393	2	AAQ10451	Hard whea
9	119.6	17.1	393	3	AAQ62457	Wheat thi
10	119.4	17.1	287	6	ABL75545	Corn tass
11	119.2	17.0	384	2	AAQ10450	Soft whea
12	118	16.9	369	3	AAQ61537	Nucleotid
13	118	16.9	369	9	AAQ59629	Barley th
14	113.6	16.2	278	7	ABX87380	Corn ear-
15	108.6	15.5	370	3	AAQ62455	Barley th
16	103.2	14.7	297	9	ADC08862	B2 PCR fr
17	100.8	14.4	366	7	ADA70643	Rice gene
18	100.6	14.4	489	3	AAQ48089	Zea mays
19	100	14.3	480	3	AAQ35542	Arabidops
20	100	14.3	524	3	AAQ38829	Arabidops
21	100	14.3	563	3	AAQ34211	Arabidops
22	99.8	14.1	574	3	AAQ51738	Catalpa s
23	98.4	14.1	357	6	ABZ13931	Arabidops

24	98.4	14.1	357	7	ADA67904	Arabidops
25	98.4	14.1	652	3	AAQ48656	Arabidops
26	97.8	14.0	614	3	AAZ51741	Vernonia
27	97.4	13.9	509	5	AAH87768	Peppermin
28	97.4	13.9	572	3	AAQ52069	Arabidops
29	96.2	13.7	601	3	AAZ51740	Glycine m
30	94.6	13.5	590	7	AAQ38792	Arabidops
31	93.6	13.4	576	7	ABX56868	Arabidops
32	93	13.3	360	6	ABZ12359	Arabidops
33	93	13.3	560	3	AAQ41961	Arabidops
34	91.8	13.1	328	3	AAQ31097	Plant mic
35	91.2	13.0	320	3	AAQ31785	Plant mic
36	91.2	13.0	594	3	AAQ48156	Zea mays
37	90.6	12.9	452	3	AAQ46727	Zea mays
38	89.8	12.8	345	6	ABZ12358	Arabidops
39	89.8	12.8	345	6	ABN89587	Arabidops
40	89.8	12.8	561	3	AAQ51522	Arabidops
41	89.8	12.8	563	3	AAQ34121	Arabidops
42	89.8	12.8	3129	6	ABN89579	Phaseolin
43	89.8	12.8	3129	6	ABN53095	DNA encod
44	89.8	12.8	3888	6	ABN89581	Phaseolin
45	89.8	12.8	3888	6	ABN89580	Phaseolin

ALIGNMENTS

RESULT 1

ADC06863

ID ADC06863 standard; DNA; 540 BP.

XX

AC ADC06863;

XX

DT 18-DEC-2003 (first entry)

XX

DE Plasmid pDONR201 containing the modified rice thioredoxin H DNA.

XX

XX cloning; recombination method; ds; plasmid pDONR201; rice; thioredoxin H.

XX Synthetic.

OS Unidentified.

OS Oryza sativa.

XX

PN US2003143618-A1.

XX

PD 31-JUL-2003.

XX

XX 23-JAN-2003; 2003US-00349782.

XX

PR 23-JAN-2002; 2002EP-00075373.

XX

XX (HATZ/) HATZFELD Y.

PA (FRAN/) FRANKARD V M.

PA (DROU/) DROUAL A.

PI Hatzfeld Y, Frankard VM, Droual A;

DR WPI; 2003-671205/63.

XX

PT Producing a modified, chimeric, or reconstructed DNA molecule of two

PT parts comprises amplifying the two DNAs by PCR using primers

PT incorporating recombination sites, ligating the PCR products, and then

PT cloning the ligated products.

XX

XX Disclosure; Fig 5; 15pp; English.

CC

CC The invention relates to a novel method for producing a modified,

CC chimeric, or reconstructed DNA molecule composed of 2 parts. The method

CC comprises PCR amplification of each part using two primer sets that build

CC in recombination sites at the outer ends of each PCR product, ligating

CC the two PCR products and cloning the ligated products into a

CC recombination vector. The method of the invention may be useful for the

CC easy cloning and selection of chimeric DNA molecules. Unlike classical

even up low  
See identity, still  
a thioredoxin h

CC recombination methods the new method avoids the need for initial cloning  
CC using restriction enzymes and allows the production of mutated and/or  
CC chimeric DNA molecules. The current sequence is that of the plasmid  
CC pDON201 of the invention which contains the modified rice thioesterase H  
CC DNA.

XX  
XX  
SQ Sequence 540 BP; 144 A; 130 C; 135 G; 131 T; 0 U; 0 Other;  
Query Match 26.9%; Score 188; DB 9; Length 540;  
Best Local Similarity 66.4%; Pred. No. 9.7e-23;  
Matches 260; Conservative 0; Mismatches 120; Indels 0; Gaps 0;  
QY 38 ATAATGCGGCGGAGGAGGAGTGGCGTGGTCCACCAAGGAGGAGTGGAGGCC 97  
DB 55 ACAATGCGGCGGAGGAGGAGTGGCGTGGTCCACCAAGGAGGAGTGGAGGCC 114  
QY 98 CGCATGCGGCGGAGGAGGAGTGGCGTGGTCCACCAAGGAGGAGTGGAGGCC 157  
DB 115 CAGATGCGGCGGAGGAGGAGTGGCGTGGTCCACCAAGGAGGAGTGGAGGCC 174  
QY 158 TGCAGTGGGTCGAGAGTGGCGGCGGAGTGGCGGAGGAGTGGAGGCC 217  
DB 175 TCGGAGCGGTCGCGTTCATCGCGGAGTGGCGGAGGAGTGGAGGCC 234  
QY 218 CGGTCTTCCTGAGGTCGAGTGGCGGAGTGGCGGAGGAGTGGAGGCC 277  
DB 235 GCTGTCTTCCTGAGGTCGAGTGGCGGAGTGGCGGAGGAGTGGAGGCC 294  
QY 278 CATGTGATGCGGAGTTCGCTTCATCAGGAGGAGGAGTGGCGGAGGAGTGGAGGCC 337  
DB 295 GAGCAATGCGGAGTTCCTTATTCATCAGGAGTGGCGGAGGAGTGGAGGCC 354  
QY 338 GTCGAGGAGGAGTGGCGGAGTGGCGGAGTGGCGGAGGAGTGGAGGCC 397  
DB 355 GCCAGGAGGAGTGGCGGAGTGGCGGAGTGGCGGAGGAGTGGAGGCC 414  
QY 398 GCTCTGCTGCGGAGTGGCGGAGTGGCGGAGTGGCGGAGGAGTGGAGGCC 417  
DB 415 GCTCTGCTGCGGAGTGGCGGAGTGGCGGAGTGGCGGAGGAGTGGAGGCC 434

## RESULT 2

AAQ78205  
ID AAQ78205 standard; cDNA; 686 BP.  
XX  
AC AAQ78205;  
XX  
XX  
DT 16-OCT-2003 (revised)  
DT 13-JUL-1995 (first entry)  
XX  
DE Gene coding for protein found in phloem sieve tube of rice.  
XX  
XX Phloem sieve tube element; plant vascular bundle; rice;  
KW protein transport; migration; fusion protein; ds.  
XX  
OS Oryza sativa; (var. aichiasahi).

XX  
XX Key Location/Qualifiers  
FH 5'UTR 1..56  
FT FT /\*tag= b  
FT CDS 57..425  
FT FT /\*tag= a  
FT 3'UTR 426..686  
FT FT /\*tag= c

JP06269286-A.

27-SEP-1994.

19-MAR-1993; 93JP-00060763.

19-MAR-1993; 93JP-00060763.

XX

(MITS-) MITSUI GYOSAI SHOKUBUTSU BIO KENKYUSHO.

WPI; 1994-346185/43.  
DR P-PSDB; AA365308.

XX Plant sieve tube protein gene - useful for transfer of useful proteins to  
XX the sieve tube.  
XX

Claim 1; Page 6; 13pp; Japanese.

XX  
XX Proteins obtained from the proboscis of a rice leaf hopper (Nilaparvata  
XX lugens Stal) were analysed; AA865909 is the partial sequence of a  
XX fragment of a protein that is transported to the sieve tube. Based on  
XX this partial amino acid sequence, a probe (AAQ78206) was designed to  
XX screen for a sequence coding for the protein. A gene was cloned from the  
XX "aichiasahi" variety of rice (AAQ78205). By fusing the gene to a sequence  
XX coding for a second useful protein, the second protein will be  
XX transported to the sieve tube. (Updated on 16-OCT-2003 to standardise OS  
XX field)

SQ Sequence 686 BP; 170 A; 150 C; 182 G; 184 T; 0 U; 0 Other;

Query Match 26.5%; Score 185.6; DB 2; Length 686;  
Best Local Similarity 66.5%; Pred. No. 2.5e-22;  
Matches 266; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

QY 18 AAGGAGAGAGAGGTCGGAATATCGCGCGGAGGAGGTCGCGTGGTGGTGGTCA 77  
DB 34 AGGAATTAGAGAGAGAGAGGCAATGCGCGCGGAGGAGGTCGCGTGGTGGTGGTCA 93  
QY 78 CCAAGGAGAGAGTTCGACGCGCGCATGCGCGCGGAGGAGGTCGCGTGGTGGTGGTCA 137  
DB 94 ACAAGGAGAGTTCGACGCGCGCATGCGCGCGGAGGAGGTCGCGTGGTGGTGGTCA 153  
QY 138 TCGACTTATGCGCGCGCGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 197  
DB 154 TTGACTTCACTGCTTCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 213  
QY 198 GCGCGGAGGAGTACCTTCTCGCGGTCCTTCTCGAGGTCGAGGTCGAGGTCGAGGTCGAGG 257  
DB 214 AGCGGAGGAGTTCCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 273  
QY 258 TCGCGAAGTTCACGCGGTCGATGCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGTCG 317  
DB 274 TTGCTGAGGAGTACAATGCGAGGCAATGCGAGGCAATGCGAGGCAATGCGAGGCAATGCG 333  
QY 318 CGCTCGAGAGCTTGTCTACCGTCGAGGAGGAGGTCGCGGAGGAGGTCGCGGAGGAGGTCG 377  
DB 334 AGGCTGAGAGGTCGTTGGCGCGGAGGAGGTCGCGGAGGAGGTCGCGGAGGAGGTCG 393  
QY 378 CCGCGCGCTGGCACTACGAGGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 417  
DB 394 TCGGTGCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 433

## RESULT 3

AAC66375  
ID AAC66375 standard; cDNA; 687 BP.XX  
AC AAC66375;  
XX

DT 23-FEB-2001 (first entry)

DE Rice thioesterase h cDNA sequence.

XX  
XX Transformed plant; transfer protein; intercellular transfer;  
KW thioesterase h; rice; ss.  
XX

OS Oryza sativa.

XX  
XX Key Location/Qualifiers  
FH 57..425  
FT CDS /\*tag= a  
FT

FT XX /product= "Thioredoxin h"  
XX JP2000262169-A.  
XX 26-SEP-2000.  
XX 19-MAR-1999; 99JP-00074914.  
XX 19-MAR-1999; 99JP-00074914.  
XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.  
XX WPI; 2000-682116/67.  
XX P-PSDB; AAB35810.  
XX Transformed plants which can control the intercellular transfer of  
XX molecules using protoplasmic connections.  
XX Example; Page 6-7; spp; Japanese.  
XX This invention relates to a method for the production of a transformed  
XX plant which contains DNA which hybridises with DNA encoding a transfer  
XX protein. The transformed plant can control the intercellular transfer of  
XX a substance through the protoplasmic connections in the plant. The  
XX present sequence represents cDNA encoding rice thioredoxin h. The cDNA  
XX sequence is used in an example illustrating the method of the invention  
XX  
XX Sequence 687 BP; 171 A; 150 C; 182 G; 184 T; 0 U; 0 Other;  
SQ  
Query Match 26.5%; Score 185.6; DB 3; Length 687;  
Best Local Similarity 66.5%; Pred. No. 2.5e-22;  
Matches 266; Conservative 0; Mismatches 134; Indels 0; Gaps 0;  
QY 18 AAGGAGAGAGGGTGGGAATAGTGGCGGAGGAGGGTCCGTGATCGGTCGCCACA 77  
DB 34 AGGAATTAGGAGGAGAGAGCAATGGCCGCGAGGAGGAGTGTGATCGCTGCCACA 93  
QY 78 CCAAGGACAGGTTCGAAGCCCGCATGGCCCAAGGCCAAGGAGGAGGCAAGCTGGTCA 137  
DB 94 ACGAGGACAGGTTCGAAGCCCGCATGGCCCAAGGCCAAGGAGGAGGCAAGCTGGTCA 153  
QY 138 TCGACTTATGGCCCTCGTGTGAGTGGTGCAGATGATGATGATGATGATGATGATGAT 197  
DB 154 TTGACTTCACTGCTTCCTGGTGGCCCTTGCCTTTCATCGCCCAAGTGTGCTGAAT 213  
QY 198 GCGCAGGAGGAGTACCTTCCTGGGCTTCCTCGAGTTCGACGAGTCTGCTGGAAG 257  
DB 214 AGCCAAAAGTTCCTGT 273  
QY 258 TCGGAGATCTACGGGTCCTATGATGATGATGATGATGATGATGATGATGATGATGAT 317  
DB 274 TTGCTGAAAAGTACATGTGCGAGCAATGCCGACCTTCCTATTTCATCAGGATGCTG 333  
QY 318 CGCTCGAGAGCTTGTCTACCGTGCAGGAGGAGGAGTCCGGAGCGCTGAGGAGTACG 377  
DB 334 AGGCTGACAGAGTGTGTGCGCGCAGGAGGAGTACCTCCAGAACACCATCTGTAAGCAG 393  
QY 378 CGCGCGCTGGCACTACGAGCGCTTCCTCGCTCGCGCTCGC 417  
DB 394 TCGTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 433  
RESULT 4  
ID ADC06864  
AC ADC06864 standard; DNA; 660 BP.  
XX  
XX ADC06864;  
XX  
XX 18-DEC-2003 (first entry)  
XX Plasmid pDONR201 containing the rice thioredoxin H DNA - alternative.  
XX cloning; recombination method; ds; plasmid pDONR201; rice; thioredoxin H.  
KW

XX Unidentified.  
OS Oryza sativa.  
XX  
XX US2003143618-A1.  
XX 31-JUL-2003.  
XX 23-JAN-2003; 2003US-00349782.  
XX 23-JAN-2002; 2002EP-00075373.  
XX (HATZ/) HATZFIELD Y.  
XX (FRAN/) FRANKARD V M.  
XX (DROU/) DROUAL A.  
XX Hatzfield Y, Frankard VM, Droual A;  
XX WPI; 2003-671205/63.  
XX Producing a modified, chimeric, or reconstructed DNA molecule of two  
XX parts comprising amplifying the two DNAs by PCR using primers  
XX incorporating recombination sites, ligating the PCR products, and then  
XX cloning the ligated products.  
XX Disclosure: Fig 2; 15pp; English.  
XX The invention relates to a novel method for producing a modified,  
XX chimeric, or reconstructed DNA molecule composed of 2 parts. The method  
XX comprises PCR amplification of each part using two primer sets that build  
XX in recombination sites at the outer ends of each PCR product, ligating  
XX the two PCR products and cloning the ligated products into a  
XX recombination vector. The method of the invention may be useful for the  
XX easy cloning and selection of chimeric DNA molecules. Unlike classical  
XX recombination methods the new method avoids the need for initial cloning  
XX using restriction enzymes and allows the production of mutated and/or  
XX chimeric DNA molecules. The current sequence is that of the plasmid  
XX pDONR201 of the invention which contains the rice thioredoxin H DNA. This  
XX sequence, located in figure 2, differs from that in the sequence listing.  
XX  
XX Sequence 660 BP; 172 A; 160 C; 159 G; 169 T; 0 U; 0 Other;  
SQ  
Query Match 26.4%; Score 184.8; DB 9; Length 660;  
Best Local Similarity 67.9%; Pred. No. 3.4e-22;  
Matches 258; Conservative 0; Mismatches 122; Indels 0; Gaps 0;  
QY 38 ATAATGGCGCGGAGGAGGGTCCGTGATCGCTGCCACACAAAGGAGGATTCGACGCC 97  
DB 127 ACAATGGCGCGGAGGAGGGAGTGTGATCGCTGCCACACAAAGGAGGATTCGACGCC 186  
QY 98 CGCATGGCCAAAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 157  
DB 187 CAGATGACCAAGGCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 246  
QY 158 TGCAGTGGGTGCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 217  
DB 247 TGTGGCCCTTGGCGCTTCATCGCCCAAGTGTGATGATGATGATGATGATGATGATGAT 306  
QY 218 GCGGTCTTCTCGAGGTGAGTGCAGCAATGCTGGAAGTGCAGAGTCTACGGCTC 277  
DB 307 GCTGTCTTCTCGAGGTGAGTGTGATGAGTGCAGAGGAGTGTGATGATGATGATGATGAT 366  
QY 278 CATGTGATGCCGACCTTCTGCTTCATCAGGAACCGCGGAGAGCTCGAGAGCTTCTAC 337  
DB 367 GAGGCAATGCCGACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 426  
QY 338 GTGCGAGGAGGAGTCCGGGAGCGCCGTGAGGAGTACGGCGCGCTGGGCACTAGGCG 397  
DB 427 GCCAGGAGGAGTACCTCCAGAACACCATCGTGAAGCAGCTCGGTGCGCACTGCTGATCT 486  
QY 398 GCTCTCTGCTCGGCGTCCGC 417  
DB 487 GCTTCTGCTGAGGAATTCTC 506







PA (INRG ) INST NAT RECH AGRONOMIQUE.  
 XX Gauthier M, Lullien-Pellerin V, De Lamotte F, Joudrier P;  
 XX WPI; 1996-117050/12.  
 XX P-PSDB; AAR93017.  
 XX New thioredoxin h from hard and soft wheat - useful e.g. as flour  
 XX additive or for inactivating toxins, also related nucleic acid, vectors,  
 XX PT transformed cells, etc.  
 XX  
 PS Claim 8; Page 34; 50pp; French.  
 XX  
 CC AAT10451 encodes hard wheat thioredoxin h (Thh). Thioredoxin h from hard  
 CC or soft wheat or other plant is useful as a food additive to improve  
 CC flour quality or to suppress the anti-nutritional effects of leguminous  
 CC plants. A further use is to inactivate toxins, esp. bee or snake venom.  
 CC cDNA clones encoding Thh (pTAM138 encodes soft wheat Thh and pTAM14132  
 CC encodes hard wheat Thh) were selected using a Thh probe which achieves  
 CC specific and accurate selection. The clones may be used in the  
 CC recombinant prodn. of Thh which produces a higher yield than extraction  
 CC from wheat. Thh contg. cells can be used directly in food processing.  
 CC (Updated on 25-MAR-2003 to correct PI field.) (Updated on 16-OCT-2003 to  
 CC standardise OS field)  
 XX  
 SQ Sequence 393 BP; 82 A; 105 C; 133 G; 73 T; 0 U; 0 Other;  
 Query Match 17.1%; Score 119.6; DB 2; Length 393;  
 Best Local Similarity 59.4%; Pred. No. 2.8e-11;  
 Matches 203; Conservative 0; Mismatches 139; Indels 0; Gaps 0;  
 QY 43 GCGCGCGGAGGAGGTCGCGTGTACGCGGACTGCGCCAGAGTTCAGACGCCCGCAT 102  
 DB 48 GCGGTGGGCGGAGGAGTCTCGTCCACAGCTGGAGCAGTGGACCATGCAGAT 107  
 QY 103 GCGCAGGCGAAGAGCGGAGTGGTGTATCGTCTCATGCTTATGCCCCCTGGTGCAG 162  
 DB 108 CGAGGAGGCCAACCGCGCCAGAGCTGGTGTGATCTGCCAAGAGTTCACGCTGCTGT 167  
 QY 163 TGGGTGCGAGATGATGGCCCCCGGTGTACGGGAGCTCGGCCAGCAAGTACCTTCGCGGT 222  
 DB 168 ACCATGCGGATCATGGCTCCAAATTTTGTGTGATCTGCCAAGAGTTCACGCTGCTGT 227  
 QY 223 CTTCCTCGAGTCGAGTCGACGAACTCTGCGAGTGGCGAGATCTACGGGCTCATGT 282  
 DB 228 TTTCTCAAGTCGACGTGTGATGAACTGAAAGCCATTGTCGACCAATTGAGCTCGAGGC 287  
 QY 283 GATGCGGACCTTCTGCTTCATCAGGAACCGCGAGAGCTCGAGAGCTTTGCTACCGTGA 342  
 DB 343 CGAGAGCGAGCTCGGGACGCCCTCAGGAGTACGCGCGCGC 384  
 DB 348 CAAGGAGGAGCTGACGACCAAGGTTGGGCTCCAGCGCGCTGC 389  
 RESULT 9  
 AAC62457  
 ID AAC62457 standard; cDNA; 393 BP.  
 XX AAC62457;  
 XX  
 DT 07-FEB-2001 (first entry)  
 XX  
 DE Wheat thioredoxin h coding sequence #2.  
 XX  
 XX Wheat; thioredoxin h; disulfide bridge reduction; development;  
 XX hair care product; venom neutralisation; food technology; food allergy;  
 XX ss.  
 XX Triticum aestivum.  
 OS  
 XX WO200058352-A2.  
 PN

XX  
 PD 05-OCT-2000.  
 XX  
 XX 31-MAR-2000; 2000WO-US008566.  
 XX  
 XX 31-MAR-1999; 99US-0127198P.  
 XX 06-DEC-1999; 99US-0169162P.  
 XX 21-JAN-2000; 2000US-0177739P.  
 XX 21-JAN-2000; 2000US-0177740P.  
 XX (REGC ) UNIV CALIFORNIA.  
 XX  
 XX Cho M, Del Val G, Caillaud M, Lemaux PG, Buchanan BB;  
 XX WPI; 2000-679291/66.  
 XX P-PSDB; AAR29249.  
 XX Recombinant or isolated nucleic acid, useful for producing transgenic  
 XX plants with altered redox properties, encode thioredoxin h or thioredoxin  
 XX reductase.  
 XX  
 XX Example 1; Fig 2; 125pp; English.  
 XX  
 CC The present invention relates to the isolation and use of the barley  
 CC thioredoxin h coding and protein sequences. These were isolated using the  
 CC corresponding sequences from wheat, one version of which is shown here.  
 CC Thioredoxin is thought to be involved in plant development via its  
 CC function in the reduction of disulfide bridges. Thioredoxin can be used  
 CC in hair care products and in the neutralisation of some venoms and  
 CC toxins, and is also useful in the reduction of some food, for example it  
 CC can be used to reduce the allergenicity of foods and the digestibility of  
 CC some proteins. It can also be used to enhance the baking qualities of  
 CC cereal flour  
 XX  
 SQ Sequence 393 BP; 82 A; 104 C; 133 G; 74 T; 0 U; 0 Other;  
 Query Match 17.1%; Score 119.6; DB 3; Length 393;  
 Best Local Similarity 59.4%; Pred. No. 2.8e-11;  
 Matches 203; Conservative 0; Mismatches 139; Indels 0; Gaps 0;  
 QY 43 GCGCGCGGAGGAGGTCGCGTGTACGCGGACTGCGCCAGAGTTCAGACGCCCGCAT 102  
 DB 48 GCGGTGGGCGGAGGAGTCTCGTCCACAGCTGGAGCAGTGGACCATGCAGAT 107  
 QY 103 GCGCAGGCGAAGAGCGGAGTGGTGTGATCGTCTCATGCTTATGCCCCCTGGTGCAG 162  
 DB 108 CGAGGAGGCCAACCGCGCCAGAGCTGGTGTGATCTGCCAAGAGTTCACGCTGCTGT 167  
 QY 163 TGGGTGCGAGATGATGGCCCCCGGTGTACGGGAGCTCGGCCAGCAAGTACCTTCGCGGT 222  
 DB 168 ACCATGCGGATCATGGCTCCAAATTTTGTGTGATCTGCCAAGAGTTCACGCTGCTGT 227  
 QY 223 CTTCCTCGAGTCGAGTCGACGAACTCTGCGAGTGGCGAGATCTACGGGCTCATGT 282  
 DB 228 TTTCTCAAGTCGACGTGTGATGAACTGAAAGCCATTGTCGACCAATTGAGCTCGAGGC 287  
 QY 283 GATGCGGACCTTCTGCTTCATCAGGAACCGCGAGAGCTCGAGAGCTTTGCTACCGTGA 342  
 DB 343 CGAGAGCGAGCTCGGGACGCCCTCAGGAGTACGCGCGCGC 384  
 DB 348 CAAGGAGGAGCTGACGACCAAGGTTGGGCTCCAGCGCGCTGC 389  
 RESULT 10  
 ABL75545  
 ID ABL75545 standard; cDNA; 287 BP.  
 XX ABL75545;  
 XX  
 DT 14-MAY-2002 (first entry)  
 XX

216 CAGGTCGCTCTTCTCTGAAGGTGACGTGGACGAA 248

RESULT 11  
 AAT10450  
 ID AAT10450 standard; cDNA to mRNA; 384 BP.  
 XX  
 AC AAT10450;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 20-SEP-1996 (first entry)  
 XX  
 XX Soft wheat thioredoxin h cDNA.  
 XX  
 XX Thioredoxin h; hard wheat; soft wheat; food additive; flour quality;  
 KW toxin inactivation; venom; ds.  
 XX  
 XX Triticum aestivum.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH 1. 384  
 FT CDS /\*tag= a  
 FT /\*product= "thioredoxin\_h"  
 FT  
 XX  
 PN WO9603505-A1.  
 XX  
 XX 08-FEB-1996.  
 XX  
 XX 26-JUL-1995; 95WO-FR001005.  
 XX  
 XX 26-JUL-1994; 94PR-0009235.  
 PR  
 XX (INRG ) INST NAT RECH AGRONOMIQUE.  
 PA  
 XX Gauthier M, Lullien-Pellerin V, De Lamotte F, Joudrier P;  
 PI WPI; 1996-117050/12.  
 DR P-PSDB; AAR93016.  
 DR  
 XX New thioredoxin h from hard and soft wheat - useful e.g. as flour  
 PT additive or for inactivating toxins, also related nucleic acid, vectors,  
 PT transformed cells, etc.  
 PT  
 PS Claim 7; Page 25-26; 50pp; French.  
 XX  
 XX AAT10450 encodes soft wheat thioredoxin h (Thh). Thioredoxin h from hard  
 CC or soft wheat or other plant is useful as a food additive to improve  
 CC flour quality or to suppress the anti-nutritional effects of leguminous  
 CC plants. A further use is to inactivate toxins, esp. bee or snake venom.  
 CC cDNA clones encoding Thh (pTAM338 encodes soft wheat Thh and pTdl4132  
 CC encodes hard wheat Thhh). The clones may be used in the  
 CC specific and accurate selection. The clones may be used in the  
 CC recombinant prodn. of Thh which produces a higher yield than extraction  
 CC from wheat. Thh contg. cells can be used directly in food processing.  
 CC (Updated on 25-MAR-2003 to correct PI field.)  
 XX  
 XX Sequence 384 BP; 84 A; 98 C; 129 G; 73 T; 0 U; 0 Other;  
 SQ

Query Match 17.0%; Score 119.2; DB 2; Length 384;  
 Best Local Similarity 59.4%; Pred. No. 3.3e-11;  
 Matches 202; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

QY 43 GCGCGCCGAGGAGGGTGCCTGTATCGCGTGCCACACCAAGACAGTTCGACGCCCGCAT 102  
 |||||  
 DB 39 GCGCGTAGGGCGGGGAGGTGATCTCCGTCCACACCTGGACAGTGGACCATGCAGAT 98  
 |||||

QY 103 GGCACAGGCCAAGAGAGAGGGCAAGCTGGTGGTTCATCGACTTATGCCCCCTTGGTGCAG 162  
 |||||

DB 99 CGAGGAGGGCCACGCCGCCCAAGAGTGGTGGTGAITGACTTCACTGCATCATGGTGGCG 158  
 |||||

QY 163 TGGGTGCCGATCATGTCGCCCGCTGTACGCGGACTCGCCGACCAAGTACCTTCCGCGGT 222  
 |||||

DB 159 ACCATCCCGCATTTATGCTTCCATTTTCGTGATTCGCCAAGAGTTCACAGCTGTGT 218  
 |||||



XX WPI: 2003-662617/62.  
DR P-PSDB; RAE39220.  
XX  
PT New transgenic plants with elevated thioredoxin levels, useful for  
PT producing plant flour or food products with reduced allergenicity and  
PT increased digestibility, or for improving seed germination that results  
PT in high yields in crops.  
XX  
PS Example 5; Fig 20; 91pp; English.  
XX  
CC The invention relates to a transgenic plant, where part(s) of the plant  
CC comprising a recombinant nucleic acid having a promoter active in such  
CC part(s) operably linked to a nucleic acid encoding a thioredoxin  
CC polypeptide, where the promoter is a seed or grain maturation-specific  
CC promoter. The transgenic plant is useful for generating plants that over  
CC express thioredoxin, as well as plants with reduced thiol groups on  
CC protein(s) such as alpha-amylase inhibitor, alpha-amylase/trypsin  
CC inhibitor, or sulphur-rich gliadin families of proteins. These proteins,  
CC such as the alpha-amylase inhibitor, are allergens that may cause  
CC allergic diseases (e.g. baker's asthma) in individuals. The transgenic  
CC plant is particularly useful for improving seed germination to establish  
CC strong growth and high yields in crop plants, or producing seeds with  
CC improved germination rates. The transgenic plant is also useful for  
CC producing plant flour and food products with reduced allergenicity and  
CC increased digestibility. The present sequence is barley thioredoxin h DNA  
XX  
SQ Sequence 369 BP; 83 A; 95 C; 119 G; 72 T; 0 U; 0 Other;  
Query Match 16.9%; Score 118; DB 9; Length 369;  
Best Local Similarity 59.1%; Pred. No. 5.2e-11;  
Matches 202; Conservative 0; Mismatches 140; Indels 0; Gaps 0;  
QY 43 GCGCGCGAGAGGTCGCGTGCACCAAGGAGGTCGAGCCCGCAT 102  
Db 21 GCGCGCGAGTGGCGGAGGTGATCTCGTCCACAGCTGGAGCAGTGCAGAT 80  
QY 103 GCGCAAGCCAGGAGGAGGCGGAGCTGTGTGTCATCGACTTCATGCGCGCGTGCAG 162  
Db 81 CGAGGAGGCGCACACCCCGAGAGCTGTGTGTGATGATGATCTGCTGATGATGTCG 140  
QY 163 TGGGTGCGAGATGATGCGCGCGGTGTACGCGAGTGTGCGCGAGTACCTTTCGCGGT 222  
Db 141 ACCATGCGCATCATGCTCCAGTTTTCGTGATCTGCGCAAGAGTTCGCAAAATCTCT 200  
QY 223 CTTCCTCGAGTCGATGTCGACGAATCTGTGGAAGTTCGCAAGATCTACGGGTTCATCT 282  
Db 201 TTCTCTCAAGTGCAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATG 260  
QY 283 GATCGCACTTCTGCTTTCATGAGGAGCGGAGAGCGCTGCGAGAGTTTGTACCGTGA 342  
Db 261 CATGCCAACGTTCTGTTTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 320  
QY 343 CGAGGAGGAGTCCGCGGAGCGCGTTCAGGAGGAGTACGCGCGCGC 384  
Db 321 CAAGGAGGAGTACCGCGGAGGAGTTCGCGTTCAGCGCGCGCGC 362  
RESULT 14  
ID ABX87380  
XX  
AC ABX87380;  
XX  
DT 24-APR-2003 (first entry)  
XX  
DE Corn ear-derived polynucleotide (cpd) #5840.  
XX  
KW Corn ear-derived polynucleotide; cdp; cDNA library; SATMON022; SATMON023;  
KW structural gene; functional gene; regulatory gene;  
KW corn ear-specific profile; gene transcription; gene expression;  
KW hybrid plant; desirable trait expression; plant breeding program;  
KW inheritance; desirable characteristic; growth; development;

XX disease resistance; environmental adaptability; quality; yield;  
KW multigene trait; plant; gene; ss.  
XX  
OS Zea mays.  
XX  
PN US6476212-B1.  
XX  
PD 05-NOV-2002.  
XX  
PF 14-MAY-1999; 98US-00313294.  
XX  
PR 26-MAY-1998; 98US-0086722P.  
XX  
PA (INCY-) INCYTE GENOMICS INC.  
XX  
PI Lalgudi RV, Ito LY, Sherman BK;  
XX WPI: 2003-208840/20.  
XX  
Novel purified corn-ear derived polynucleotide useful as hybridization  
XX probe for detecting polynucleotide in sample, and for identifying,  
XX evaluating, and altering desired characteristics associated with growth,  
XX development.  
XX  
PS Example; SEQ ID NO 5840; 390pp; English.  
XX  
CC The present invention relates to the isolation of corn ear-derived  
CC polynucleotides (cdps) from the corn (Zea mays) cDNA libraries SATMON022  
CC and SATMON023. Some of the cdps uniquely identify structural, functional,  
CC and regulatory genes of corn ear. The polynucleotide sequences are  
CC useful for detecting cdps in a sample, for producing a corn ear-specific  
CC profile of gene transcription, for detecting altered gene expression in  
CC inbred or hybrid plants, and for screening several molecules for specific  
CC binding to the polynucleotide. The cdps are useful to identify, isolate,  
CC or extend identical or related corn-ear nucleic acid sequences from DNA  
CC libraries, and in nucleic acid amplification or hybridization techniques  
CC to follow the expression of desirable traits through plant breeding  
CC programs. Preferably, the cdps are used to identify, evaluate, alter, or  
CC follow the inheritance of desired characteristics associated with growth  
CC and development, disease resistance, environmental adaptability, quality,  
CC and yield of corn. The cdps are also useful as molecular markers for  
CC studying inheritance and multigene traits in a plant breeding program.  
CC The cdps are useful for producing purified corn-ear polypeptides by  
CC recombinant techniques. They are also useful in diagnostic assays to  
CC detect or confirm conditions or diseases associated with abnormal levels  
CC of cdp expression. ABX81541-ABX89140 represent corn ear-derived  
CC polynucleotides (cdps) of the invention. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from the USPTO web site at  
CC seqdata.uspto.gov/psids/IDEntry.html  
XX  
SQ Sequence 278 BP; 66 A; 82 C; 81 G; 48 T; 0 U; 1 Other;  
Query Match 16.2%; Score 113.6; DB 7; Length 278;  
Best Local Similarity 71.6%; Pred. No. 2.8e-10;  
Matches 149; Conservative 0; Mismatches 59; Indels 0; Gaps 0;  
QY 36 GAATAATGGCGCGGAGGAGGTGCGGTGATCGCGTCCACCAAGGAGGAGTTCGACG 95  
Db 41 GATCAATGGGTGCGAGCGGAGTGTGATCGGTGCCACAGAGGCTGAGTTCGACG 100  
QY 96 CCGCATGGCCCAAGGCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 155  
Db 101 CCCATGACCAAGGCCAAGGCCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 160  
QY 156 GGTGAGTGGGTGCCAGATGATGCGCGGTGTACCGGAGTCCGCCAGCAAGTACCCCT 215  
Db 161 GGTGCGGTCCATGCGCGGCGCATGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 220  
QY 216 CCGCGGTCTTCCTCGAGGTCGAGTCGAGTGA 243  
Db 221 AGGTGCGTCTTCCTCGAGGTCGAGTCGAGTGA 248

## RESULT 15

AAC62455 standard; cDNA; 370 BP.

XX AAC62455;

XX 07-FEB-2001 (first entry)

XX Barley thioedoxin h coding sequence.

DE Barley; thioedoxin h; disulfide bridge reduction; development;

KW hair care product; venom neutralisation; food technology; food allergy;

KW ss.

XX Hordeum vulgare.

XX WO2000058352-A2.

XX 05-OCT-2000.

XX 31-MAR-2000; 2000WO-US008566.

XX 31-MAR-1999; 99US-0127198P.

PR 06-DEC-1999; 99US-0169162P.

PR 21-JAN-2000; 2000US-017719P.

PR 21-JAN-2000; 2000US-017740P.

XX (REGC ) UNIV CALIFORNIA.

XX Cho M, Del Val G, Caillau M, Lemaux PG, Buchanan BS;

XX WPI; 2000-679291/66.

DR P-PSDB; AAB23247.

XX Recombinant or isolated nucleic acid, useful for producing transgenic plants with altered redox properties, encode thioedoxin h or thioedoxin reductase.

XX Claim 60; Fig 2; 125pp; English.

XX The present invention relates to the isolation and use of the barley thioedoxin h coding and protein sequences, the former of which is shown here. These were isolated using the corresponding sequences from wheat. Thioedoxin is thought to be involved in plant development via its function in the reduction of disulfide bridges. Thioedoxin can be used in hair care products and in the neutralisation of some venoms and toxins, and is also useful in the reduction of some food, for example it can be used to reduce the allergenicity of foods and the digestibility of some proteins. It can also be used to enhance the baking qualities of cereal flour

SQ Sequence 370 BP; 83 A; 95 C; 119 G; 73 T; 0 U; 0 Other;

Query Match 15.5%; Score 108.6; DB 3; Length 370;

Best Local Similarity 59.2%; Pred. No. 1.9e-09;

Matches 203; Conservative 0; Mismatches 139; Indels 1; Gaps 1;

QY 43 GCGGCCGAGGAGGTGCGTGTATCGC-GTCCACACCAAGCAGAGTTGCAACCCGCA 101

DB 21 GCGGCCAGTGGCGGGAGGTGATCTCGTTCCACAGCTGGAGCAGTGGACCATGCAGA 80

QY 102 TGGCCACGCCCAAGCAGGCGAGCTGTGTATCGTCTCATGCCCCCTGTGTCA 161

DB 81 TCGAGGAGGCCAACACCCCAAGAGCTGGTGGTGAATGACTTCACTCATCATGTGGCG 140

QY 162 GTGGGTGTCAGATATGCCCCGGTGTACGGGAGTGGCCAGCAAGTACCCCTTCGCGG 221

DB 141 GACCATGCGCATCATGCTCCAGTTTTCGTGTATCTGCCAAGAAGTTCCAAATGCTG 200

QY 222 TCTTCTCGAGTGCAGCTGTGACGAGCTGTGAGAGTGGGAGATCTACCGGTCCATG 281

DB 201 TTTTCTCAAGTGCAGCTGGATGAACCAATGCTGAGCAATTCAGTGTGAGG 260

QY 282 TGATGCCGACCTTCTGCTTCATCAGGACGGCGAGACGCTCGAGAGCTTTGCTACCGTCG 341  
 DB 261 CCATGCCCAACGTTCTCTGTTTCATGAGGAAGGAGAGCGTCAAGGACAGGGTTGTCGGAGCTA 320  
 QY 342 ACGAGGACGAGCTCCGGGACGCCGCTCAGGAAGTACGCCGCCCGC 384  
 DB 321 TCNAGGAGGAACTGACCGGCCAAGGTTGGGCTTCACGGCGGCGGC 363

Search completed: May 5, 2004, 21:08:21

Job time : 314.462 secs

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	195.2	27.9	466	6	AR414207	AR414207 Sequence
2	195.2	27.9	466	6	BD109760	BD109760 EST and e
3	187	26.7	601	8	OSU92541	OSU92541 Oryza sativ
4	185.6	26.5	600	8	AK059196	AK059196 Oryza sat
5	185.6	26.5	600	8	E08194	E08194 RPS13 gene
6	185.6	26.5	686	8	E08194	E08194 RPS13 gene
7	185.6	26.5	686	8	E08194	E08194 RPS13 gene
8	184	26.3	526	11	G73679	G73679 R248R etio
9	165.6	23.7	598	8	AY072771	AY072771 Trifolium
10	162.4	23.2	357	8	AY245454	AY245454 Hordeum v
11	137.2	19.6	318	6	AR250509	AR250509 Sequence
12	123.4	17.6	664	8	AF323593	AF323593 Prunus pe
13	121.2	17.3	596	8	TA89762	TA89762 Trifolium
14	120.6	17.2	371	11	G71188	G71188 V8028311FM
15	119.6	17.1	393	6	A48516	A48516 Sequence 4
16	119.6	17.1	437	8	AF420472	AF420472 Trifolium
17	119.6	17.1	630	6	A48520	A48520 Sequence 8
18	119.6	17.1	630	8	TDAJ1903	TDAJ1903 Trifolium
19	119.2	17.0	384	6	A48514	A48514 Sequence 2
20	119.2	17.0	393	8	AF286593	AF286593 Trifolium
21	119.2	17.0	629	8	TA840845	TA840845 Trifolium
22	119.2	17.0	659	8	A48519	A48519 Sequence 7
23	119.2	17.0	670	8	TATHIORDH	TATHIORDH
24	118	16.9	320	8	RICSS396	RICSS396
25	118	16.9	369	8	AY245455	AY245455 Hordeum v
26	115	16.4	1285	8	CRTRXH	CRTRXH
27	114	16.3	676	8	AY344230	AY344230 Ipomoea b
28	113.6	16.2	278	6	AR250481	AR250481 Sequence
29	105	15.0	720	8	BT009180	BT009180 Trifolium
30	102.4	14.6	580	8	BNUS9380	BNUS9380 Brassica na
31	102.2	14.6	463	8	AF273844	AF273844 Brassica
32	102.2	14.6	535	8	AB010434	AB010434 Brassica
33	102.2	14.6	544	8	BOPC17	BOPC17
34	102.2	14.6	554	8	BNUS9379	BNUS9379 Brassica na
35	101.8	14.5	740	8	AB053294	AB053294 Oryza sat
36	100.8	14.4	366	8	AK654096	AK654096 Sequence
37	100.8	14.4	682	8	AK059385	AK059385 Oryza sat
38	100.8	14.4	3740	8	AK106758	AK106758 Oryza sat
39	100.6	14.4	130372	2	CNS08C92	CNS08C92
40	100	14.3	639	8	AY085117	AY085117 Arabidops
41	99.8	14.3	784	8	AY271308	AY271308 Citrus x
42	98.4	14.1	357	6	AX412276	AX412276 Sequence
43	98.4	14.1	357	6	AX412277	AX412277 Sequence
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ALIGNMENTS

RESULT 1  
AR414207  
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DEFINITION Sequence 1844 from patent US 6639063.  
ACCESSION AR414207  
VERSION AR414207.1 GI:40169317  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 466)  
AUTHORS Edwards, J.-B.D.M., Jobert S. and Giordano, J.-Y.  
TITLE EST's and encoded human proteins  
JOURNAL Patent: US 6639063-A 1844 28-OCT-2003;  
FEATURES Location/Qualifiers

OM nucleic - nucleic search, using sw model  
Run on: May 5, 2004, 13:19:01 ; Search time 2847.79 Seconds  
(without alignments)  
10653.920 Million cell updates/sec  
Title: US-10-005-429-13  
Perfect score: 700  
Sequence: 1 ggatccacacgaggaag.....aaaaaaaaaaaaaaaaaaaaa 700  
Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0  
Searched: 3470272 seqs, 21671516995 residues  
Total number of hits satisfying chosen parameters: 6940544  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
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1: gb.ba.\*  
2: gb.htg.\*  
3: gb.in.\*  
4: gb.in.\*  
5: gb.ov.\*  
6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*  
15: em.ba.\*  
16: em.fun.\*  
17: em.hum.\*  
18: em.in.\*  
19: em.mu.\*  
20: em.or.\*  
21: em.or.\*  
22: em.ov.\*  
23: em.pat.\*  
24: em.ph.\*  
25: em.pl.\*  
26: em.ro.\*  
27: em.sts.\*  
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30: em.htg.hum.\*  
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34: em.htg.pin.\*  
35: em.htg.rod.\*  
36: em.htg.mam.\*  
37: em.htg.vrt.\*  
38: em.sv.\*  
39: em.htgo.hum.\*  
40: em.htgo.mus.\*  
41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a

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Query Match	27.9%;	Score 195.2;	DB 6; Length 466;
Best Local Similarity	72.0%;	Pred. No. 9.9e-22;	
Matches 268;	Conservative	0;	Mismatches 103; Indels 1; Gaps 1;
QY	36	GAATAATGCGCGCCGAGGAGGTGCGTGATCGGTGCCACACCAAGGACGAGTTGCAAGC	95
Db	66	GATCAATGGCGTCCGAGCAGGAGTGTGTCATCGGTGCCACAGCAAGGCTGAGTTGCAAGC	135
QY	96	CCGCGATGCGCAAGGCCAAGGACGAGGCGCAAGCTGCTGTGTCATCGACTTCATGGCCCCCT	155
Db	126	CCCAATGATCCAAAGGCCCAAGGAAGCCGCGAAGCTGTGTGTCATCGACTTCACATGCCGCT	185
QY	156	GGTGCATGGGTGCCAGATGATGAGGCCCGGTGTACGGGACTGTGGCGCAGCAAGTACGCTT	215
Db	186	GGTGC-GTCCATGCGCGGCCATCGGCCCACTGTTCGTGAAACACGCCAAGAAGTTCACCTC	244
QY	216	CGCGGTCTTCTCGAGGTGCAAGCTCGACAACTGCTGGAAGTCGCGAAGATCTACGGCG	275
Db	245	AGGTGCTTCTCTGAAGTGGACGTGGACGAAGTGAAGGAAGTCAACGGGCCCTACGAGG	304
QY	276	TGCATGTGATGCGCACTTCTGCTTCATCAGGAACGGCGAGAGCTCGAGAGTTTGCTA	335
Db	305	TCGAGCGATGCCGACCTTCCACTTCGTCAAGAACGCCAAGACGGTCGCAACATCGTGG	364
QY	336	CGGTGACGAGACGAGCTCCCGGACGCCGTCAAGGAAGTACGCCCGCGCTGGCACTACGA	395
Db	365	GTGCCAGGAAGCAGAGCTCTCGGCCAGATCGAAGCATGCGCGCCTGCGCCTGCGT	424
QY	396	CGGCTCTCGCT	407
Db	425	CTGCGTCTCGCT	436

```

RESULT 3
OSU92541
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

OSU92541
Oryza sativa thioredoxin h mRNA, complete cds.
601 bp mRNA linear
PLN 09-APR-1997

Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 601)
Lee,N.C.; Eun,M.Y. and Lee,G.R.
Isolation and characterization of thioredoxin h gene from rice
Unpublished
2 (bases 1 to 601)
Lee,M.C. and Eun,M.Y.
Direct Submission
Submitted (09-MAR-1997) Cyto genetics, National Institute of
Agricultural Science and Technology, Se-bun Dong, Suwon 440-707,
Korea

FEATURES
source
1..601
Location/Qualifiers
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    /mol_type="mRNA"
    /strain="Wilyang 23"
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    /clone="KCDL766"
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    /product="thioredoxin h"
    /protein_id="AA851522.1"
    /db_xref="GI:1930072"

CDS

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/translation="MAAERGWIACHNKFDEFAQMTKAKEAGKVWIIDFTASWGCPCT  
 FTAPVFAEYAKFPFGAVFLKVDVDELKEVAEKNVEMPTFLFKDGAEDKVGKARG  
 DDLQNTIVXEVGATAASA"

ORIGIN

Query March 26.7%; Score 187; DB 8; Length 601;  
 Best Local Similarity 65.9%; Pred. No. 2,1e-20;  
 Matches 271; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

QY 7 CACACGAGAAAGGAGAGAGAGAGGTCGGAATAATGCGGCGCCGAGAGGGTGCCTGAT 66  
 DB 52 CTCGTCCCGAGGGAATTAGGAGGAGAGAGCAATGGCGCGCGAGAGGGATGCTGTGAT 111  
 QY 67 CGCGTCGCCACACCAAGGACGAGTTCGACGCCCCATGGCCAAAGGCCAAGAGCAGAGGCA 126  
 DB 112 CGCTCCGACCAAGAGGAGCGGTTTCGACGCCAGATGACCAAGGCCAAGAGGAGCGCGCA 171  
 QY 127 GCTGCTGGTTCATCGACTTCATGCGCCCCCTGGTGTCTGATGGGTGCCAGATGATGCGCCGGT 186  
 DB 172 AGTGGTGCATAATTCGACTTCATGCTCTTCCTGGTGTGGCCCTTGGCGCTTATCGCCCACT 231  
 QY 187 GTACCGGAGCTCGCCGAGCAAGTACCCCTTCCGCGGCTCTTCCCTCGAGTGCAGCTCGAGCA 246  
 DB 232 GTTCGTGAATACGCCCAAAAGTCCCTGCTGCTCTTCCCTAGGTTGATGTTGATCA 291  
 QY 247 ACTGCTGGGAAGTCGGAAGATCTACGGCTGCATGTGATGCGGACCTTCTGCTTTCATGAG 306  
 DB 292 GCTGAAGGAAGTGTCTGAAAGTACAAATGTGAGGCAATGCCGACCTCTCTATTATCAAC 351  
 QY 307 GAACCGCGGAGAGCTCGAGAGCTTTTGCTACCTTCGACGAGGAGCAGCTCCGGGAGCGCCGT 366  
 DB 352 GGATGCTGTGAGGCTGACAAGTCTGTGGCGCCAGGAAGGATGACCTCCAGAACACCAT 411  
 QY 367 CAGGAGATACCGCGCGCTGGCACTACGAGGCTCTGCTCGGAGTCCGC 417  
 DB 412 CQTGAAGCACTCGGCGCACCTGCTGCTCATCTGCTCTGCTTGAAGTATCTC 462

RESULT 4  
 LOCUS AK059196  
 DEFINITION Oryza sativa (japonica cultivar-group) cDNA clone:001-024-A03, full insert sequence.  
 ACCESSION AK059196  
 VERSION AK059196.1 GI:32969214  
 KEYWORDS FLI CDNA; oligo-capping.  
 SOURCE Oryza sativa (japonica cultivar-group)  
 ORGANISM Oryza sativa (japonica cultivar-group)  
 Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae; Oryza.

REFERENCE 1  
 AUTHORS The Rice Full-length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team.; Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group; Otsomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kurotaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Nariikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niihara,J., Ikeda,R., Ishibiki,J., Kawakata,M., Yoshimura,K., Miura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN., Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S., Kaga,A., Hashidume,M., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M., Saito,A., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Yoshino,M., Sasaki,D., Sato,K., Shibata,K., Shingawa,A., Shiraki,T., Yoshino,M. and Hayashizaki,Y.  
 Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice  
 JOURNAL MEDLINE  
 301 (5631), 376-379 (2003)  
 22752273

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QY 78 CCAAGACAGGAGTTCAGACGCCCCGATGGCCAGGCGCAAGAGGAGGAGTGGTGTCA 137
Db 131 ACAAGACAGGAGTTCAGACGCCCCGATGGCCAGGCGCAAGAGGAGGAGTGGTGTCA 190
QY 138 TCGACTTCATGCGCCCCCTGGTGCAGTGGGTGCAGATGATGCGCCCGGCTGACGCGACT 197
Db 191 TTGACTTCATGCTTCTGGTGTGGCCCTTGGCGCTTCATCGCCCGGCTGCTGAAT 250
QY 198 GCGCCAGCAAGTACCTTCCGCGCTTCCTCGAGTGCAGTGCAGCAACTGCTGGAAG 257
Db 251 AGCCCAAAGTTCCTGGTGTGCTTCTCGAAGTTCAGTTCAGTGCAGTGAAGGAAG 310
QY 258 TCGCAGAGATACGCGCGTCCATGTGATGCCGACCTTCTGCTTCATCAGGAACGCGCAGA 317
Db 311 TTGCTGAAAGTACAATGTGAGGCAATGCCGACCTTCTATTCATCAAGGATGGTGTG 370
QY 318 CCGTCGAGAGCTTCTACCGTCGACGAGGAGGAGTCCGGGCGCGCTCAGGAAAGTACG 377
Db 371 AGCTGACAAGTGTGCTGCGCCAGAAAGATGACCTCCAGAACACCATCTGTAAGCAGC 430
QY 378 CCGCGCTGGCACTACGAGCGCTCTGCTCGCGCTCGCGTCCGC 417
Db 431 TCGGTGCCACTCTGATCTGCTTCTGCTAAGATTCTC 470

RESULT 5
LOCUS E08194
DEFINITION RPS13 gene encoding sieve tube protein.
ACCESSION E08194
VERSION E08194.1 GI:2176315
KEYWORDS JP 1994269286-A/1.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 686)
AUTHORS Kayano,M.
TITLE SIEVE TUBE PROTEIN GENE OF PLANT AND METHOD FOR MAKING USEFUL
JOURNAL PROTEIN TRANSMIGRATE TO SIEVE TUBE USING THE SAME
COMMENT PATENT: JP 1994269286-A 1 27-SEP-1994;
MITSUI GIYOUSAI SHOKUBUTSU BIO KENKUSHO:KK
OS Oryza sativa L., var. aichiasahi
PN JP 1994269286-A/1
PD 27-SEP-1994
PI 13-MAR-1993 JP 1993060763
PC C12N15/29,A01H5/00,C12P21/02//C12N5/10;
CC strandedness: Double;
CC topology: Linear;
CC Feature is identified by chter;
FH Key Location/Qualifiers
FT source 1..686
FT FT /organism='Oryza sativa L., var. aichiasahi',
FT FT /tissue_type='leaf',
FT FT /clone='CRSP13-1',
FT FT 1..56
FT 5'UTR 1..56
FT CDS 57..425
FT /products='sieve tube protein' FT 3'UTR
FT 426..686.
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source Location/Qualifiers
1..686
/organism='unidentified'
/mol_type='genomic RNA'
/db_xref='taxon:32644'

ORIGIN
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Best Local Similarity 66.5%; Pred. No. 3.6e-20;
Matches 266; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

QY 18 AAGGAGAGAGAGGAGGAGTTCGGAATATGCGCGCGGAGGAGGAGTGGCGTGCATCGGTGCCACA 77

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Db 34 AGAATTAGGAGGAGAGAGCAATGGCCGCGCGAGGAGGAGTGGTATCGCTGCCACA 93
QY 78 CCAAGGAGAGTTCGACGCCCCGATGGCCAGGCGCAAGAGGAGGAGTGGTGTCA 137
Db 94 ACAAGGAGAGTTCGACGCCCCGATGGCCAGGCGCAAGAGGAGGAGTGGTGTCA 153
QY 138 TCGACTTCATGCGCCCCCTGGTGCAGTGGGTGCAGATGATGCGCCCGGCTGACGCGACT 197
Db 154 TTGACTTCATGCTTCTGGTGTGGCCCTTGGCGCTTCATCGCCCGGCTGCTGAAT 213
QY 198 GCGCCAGCAAGTACCTTCCGCGGTCTTCTCGAGTGCAGTGCAGCAACTGCTGGAAG 257
Db 214 AGCCCAAAGTTCCTGGTGTGCTTCTCGAAGTTCAGTTCAGTGCAGTGAAGGAAG 273
QY 258 TCGCAGAGATACGCGCGTCCATGTGATGCCGACCTTCTGCTTCATCAGGAACGCGCAGA 317
Db 274 TTGCTGAAAGTACAATGTGAGGCAATGCCGACCTTCTATTCATCAAGGATGGTGTG 333
QY 318 CCGTCGAGAGCTTCTACCGTCGACGAGGAGGAGTCCGGGCGCGCTCAGGAAGTACG 377
Db 334 AGCTGACAAGTGTGCTGCGCCAGAAAGATGACCTCCAGAACACCATCTGTAAGCAGC 393
QY 378 CCGCGCTGGCACTACGAGCGCTCTGCTCGCGCTCGCGTCCGC 417
Db 394 TCGGTGCCACTCTGATCTGCTTCTGCTAAGATTCTC 433

RESULT 6
LOCUS R1CTH
DEFINITION Oryza sativa (japonica cultivar-group) mRNA for thioredoxin h, complete cds.
ACCESSION D21836
VERSION D21836.1 GI:426441
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
REFERENCE 1 (bases 1 to 687)
AUTHORS Ishiwatari,Y., Honda,C., Kawashima,I., Nakamura,S., Hirano,H., Mori,S., Fujiwara,T., Hayashi,H. and Chino,M.
TITLE Thioredoxin h is one of the major proteins in rice phloem sap
JOURNAL Planta 195 (3), 456-463 (1995)
MEDLINE 95218606
PUBMED 7766047
AUTHORS Ishiwatari,Y.
TITLE Direct Submission
JOURNAL Submitted (28-OCT-1993) Yutaka Ishiwatari, The University of Tokyo, Faculty of Agriculture, Department of Agricultural Chemistry, 1-1-1 Yayoi, Bunkyo-ku, Tokyo 113, Japan (Tel:81-3-3812-2111(ex.5105), Fax:81-3-3812-0544)
FEATURES
source Location/Qualifiers
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/organism='Oryza sativa (japonica cultivar-group)'
/mol_type='mRNA'
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/note='Clones CRPS13-312 and CRPS13-322'
57..425
/note='encoding rice phloem sap 13kD protein-1'
/codon_start=1
/product='thioredoxin h'
/protein_id='BA04864.1'
/db_xref='GI:426442'
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ORIGIN



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related information concerning this probe, please refer to the
Gramene database at http://www.gnome.jp/
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        /db_xref="taxon:39946"
        /map="7"
        /clone="RZ488"
        /clone_lib="etiolated leaf tissue of rice"
        /note="Vector: Lambda ZAP II/pBluescript; V-type: Plasmid;
A Lambda ZAP II cDNA library was constructed from mRNA
extracted from etiolated leaf tissue of the rice cultivar
'IR36' and converted to pBluescript (amp resistant) as
described in Causse et al. (1994) Genetics 138:1251-1274.
For insert amplification, Use M13 forward and reverse
primers. Restriction site is EcoRI. Clones from this
library are designated with the prefix 'RZ'."
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Query Match 26.3%; Score 184; DB 11; Length 526;  
Best Local Similarity 66.2%; Pred. NO. 6.3e-20;  
Matches 265; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

18	AAGGAGAGAGAGAGGTCGGAAATAATGGCGCGCGAGAGAGGTCGGTATATCGCTGCGACA	77
60	AGCAATTAGAGGAGAGAGAGCAATGGCCGCGCGAGAGAGGAGTCGTGATCGCTCGCCACA	119
78	CCAAAGGACGAGTTTCAGACGCCCGCATGGCCCAAGGCCAAAGGAGCAGGGCAAGCTGGTGCTCA	137
120	ACRAGGACGAGTTTCAGACGCCCGCATGATGACCAAGGCCAAGGAGGCCGCGCAAGTGGTCATAA	179
138	TCGACTTCATGGCCCCCTGGTGCGAGTGGGTGCCAGATGATGGCCCCGGGTGTACCGCGACT	197
180	TTGACTTCACTGCTCTCTGGTGGCCCTTGGCGGTTTCATGGCCCCAGATGTTCGCTGAAT	239
198	GCGCCAGCAAGTACCTTCCGGGCTCTTCCTCGAGGTCGACGTCGACGCAAGCACTCTCTGAGAG	257
240	AGCCCAAAAGTTCCCTGGTGCTGCTTCTCGAAGGTTGATGTTGATGAGCTGAAGGAAG	299
258	TCGCGAAGATCTACGGGCTCCAATGATGATGCCCACTTCTGCTTCATCAAGAACGGCGAGA	317
300	TTGCTGAAAAGTACAAATGTTGAGGCCAATGCCACCTTCTCTATTCAATCAAGGATGGTGCTG	359
318	CGCTCGAGAGCTTTCCTACCTCCGTCGAGGAGCGAGCTCCGGGAGCGCGCTCAGGAATACG	377
360	AGCTGTGACAGGTCGTTGGCGCCAGGAGAGATGACCTTCAGAAACCACTCGTGAAGCAG	419
378	CGCGCGCTGGCACTACGACGGCTCCTGCTCGCGCGCTCCG	417
420	TCGGTGCCCACTGCTGCATCTGCTTCTGCTTAAGAAATCTC	459

RESULT 9  
AY072771  
LOCUS  
DEFINITION  
ACCESSION

VERSION	AY072771.1	GI:27461139
KEYWORDS		
SOURCE		
ORGANISM		
REFERENCE		
		Triticum aestivum (bread wheat)
		Triticum aestivum
		Triticum aestivum
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Triticum.
		1 (bases 1 to 598)

REFERENCE	1 (bases 1 to 598)
AUTHORS	Cazalis, R.
TITLE	Triticum aestivum thioredoxin H
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 598)

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AUTHORS      Maeda, K., Finnie, C., Ostergaard, O. and Svensson, B.
TITLE        Direct Submission
JOURNAL      Submitted (27-FEB-2003) Chemistry, Carlsberg Laboratory, Gamle
              Carlsberg Vej 10, Copenhagen DK-2500 Valby, Denmark
FEATURES     Location/Qualifiers
              1..357
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              1..357
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Query Match

Query Match	23.2%;	Score 162.4;	DB 8;	Length 357;
Best Local Similarity	69.6%;	Pred. No. 1.8e-16;		
Matches 220;	Conservative 0;	Mismatches 96;	Indels 0;	Gaps 0;
41	ATGCGGCGCAGGAGGGTCCGCTGATCCGTGCCACACCAAGGACGAGTTTCGACGCCGC	100		
1	ATGCGGCGCAGGAGGGACCGTTATCCGTGCCACACCAAGGACGAGTTTCGATACCCAC	60		
101	ATGGCCAAAGGCCAAGGACGAGGCGAAGCTGGTGGTCATTCGATTCGGCCCCCTGGTGC	160		
61	ATGGCCAAATGGCAAGGACACCGCGCAAGCTGGTGGATCATTTGATTTTCACTGCCTCTGGTGC	120		
161	AGTGGGTGCCAGATGATGCGCCCGGTGTACCGGAGCTCGCCGACGAAGTACCCCTTCCCGCG	220		
121	GGTCATGTCGTGTGCATAGCCCCAGTCTTTGCTGAGTACGCCAAGAGTTCCTGGGGCC	180		
221	GTCTTTCTTCGAGGTGCAAGTCCGAGAACTGCTGGAACTCGCGAAGATCTACGGCGTCCAT	280		
181	ATCTTCTGAAAGTGGATGTTGATGAGCTGAAGGACGTCGCTGGAAGCATACAATGTTGAG	240		
281	GTGATGCCGACCTTCTGCTTCATCAGGAACGGCGAGCGCTCGAGAGCTTTGCTACCGTTC	340		
241	GCAATGCCGACCTTCTGCTTTTATCAAGGACCGTGAAGAGGTGGACAGTGTGTTCGGTGGC	300		
341	GACGAGGACGAGCTCC	356		
301	AGGAGGATGACATCC	316		

AR250509

### DEFINITION

NOT FOR  
SUBMISSION

ORGANISMS

## REFERENCE

FILE  
TOWENT

**SOURCE**

Qigong Master

Best Local Similarity 73.1%; Pred. No. 1.9e-12; Indels 2; Gaps 1; Matches 190; Conservative 0; Mismatches 58;

QY 36 GAATATGCGGCGGAGGAGGTCGATCGCGTGCACACCAAGGACGAGTTGCGAG 95

Db 55 GATCAATGCGGTCGAGACAGGAGTGTGATCGGTGCCACAGCAGGTCGATTCGAG 114

QY 96 CCGCATGCGCCAGGCAAGGACGAGGCAAGTGTGTGTCATCGACTTCATGCGCCCTT 155

Db 115 CCCACATGACCAAGGCCAGGAGCGGCAAGTGTGTGTCATCGACTTCATGCGCGCT 174

QY 156 GGTGCAATGCGGTCAGATGATGCGCCCGGTGTACCGGACTGCGCCAGCAATGACCTT 215

Db 175 GGTGCGGTCATGCGCGGCGCATCGCCCGCTGTTCTGACACGCGCAAGATTCACATC 234

QY 216 CCGCGGTCTTCCTCGAGGTCGAGTCGACGAACTGCTGGAAGTGGCGAAGATTCAGCGG 275

Db 235 AGTGTCTTCCTGAGGTCGAGTCGACGAACTGCTGGAAGTGGCGAAGATTCAGCGG 292

QY 276 TCCATGTGATGCGGACCTTC 295

Db 293 TCGAGGCGATGCGCGACCTTC 312

RESULT 12

AF323593

LOCUS Prunus persica thioiredoxin H mRNA linear PLN 02-NOV-2001

DEFINITION Prunus persica thioiredoxin H mRNA, complete cds.

ACCESSION AF323593

VERSION AF323593.1 GI:16588842

KEYWORDS Prunus persica (peach)

SOURCE Prunus persica

ORGANISM Prunus persica

REFERENCE 1 Callahan,A.M., Morgens,P.H. and Cohen,R.A. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus. 1 (bases 1 to 664)

AUTHORS Callahan,A.M., Morgens,P.H. and Cohen,R.A.

TITLE Isolation and initial characterization of cDNAs for mRNAs regulated during peach fruit development

JOURNAL J. Am. Soc. Hortic. Sci. 118, 531-537 (1993)

REFERENCE 2 (bases 1 to 664)

AUTHORS Callahan,A.M., Morgens,P.H., Cohen,R.A. and Scorza,R.

TITLE Regulation of peach gene expression in a peach/almond hybrid Upublished

JOURNAL 3 (bases 1 to 664)

AUTHORS Callahan,A.M., Dunn,L.L. and Cohen,R.A.

TITLE Direct Submission

JOURNAL Submitted (22-NOV-2000) USDA-ARS, Appalachian Fruit Research Station, 45 Wiltshire Rd., Kearneysville, WV 25430, USA

FEATURES

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/organism="Prunus persica"

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/db\_xref="GI:16588843"

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CDS

Query Match 17.6%; Score 123.4; DB 8; Length 664; Best Local Similarity 58.2%; Pred. No. 3.4e-10; Indels 0; Gaps 0; Matches 217; Conservative 0; Mismatches 156;

QY 46 GGCGGAGGAGGTCGCGTGTGTCGCGTGCACACCAAGGACGAGTTTCGACGCCCGCGATGC 105

Db 73 GGCGGAGGAGGTCGCGTGTGTCGCGTGCACACCAAGGACGAGTTTCGACGCCCGCGATGC 132

QY 106 CAAGCCCAAGGAGGAGGTCGCGTGTGTCGCGTGCACACCAAGGACGAGTTTCGACGCCCGCGATGC 165

Db 133 TAAGGGAACGAGAACCAAGAACTGGTGTGTCGCGTGCACACCAAGGACGAGTTTCGACGCCCGCGATGC 192

QY 166 GTGCCAGATGATGTCGCCCGGTGTAGCGGACTGCGCCAGCAAGTACCTTCGCGCGGTCTT 225

Db 193 GTGCCGTTGATGTCGCCCGGTGTAGCGGACTGCGCCAGCAAGTACCTTCGCGCGGTCTT 252

QY 226 CCGTCCAGGTCGACGTCGACGAACTGCTCGGAAGTTCGCGGAGTTCACGCGGTTCATGTGAT 285

Db 253 CCTAAGGTCGACGTCGAGTGAACCTGAGGACTGTTTCCGAGGAGTGGGGTGTGGAGGCAAT 312

QY 286 GCGGACCTTCGCTTCATCAGGACGCGGAGGAGCTTCGAGAGCTTTCCTACCGTCGACGA 345

Db 313 GCGTACCTTCCTTCCTCAAGGAGGCAAGTATGACGAGTTTGGGTGCCAAGA 372

QY 346 GGACGAGTCCCGGACGCGGTCGAGGAGTACGCGCGCTGCGACCTACGACGCGTCTCTGC 405

Db 373 AGACGAGTTACAGATCAAGTTGCGCAAGCATGTCGCGCTGCGCGCTGCGCTCGCCAC 432

QY 406 CTCGCGGTCGCGC 418

Db 433 CTCGCTCTGCGC 445

RESULT 13

TA9762

LOCUS Triticum aestivum mRNA for thioiredoxin H.

DEFINITION Triticum aestivum mRNA for thioiredoxin H.

ACCESSION AJ009762

VERSION AJ009762.1 GI:4138593

KEYWORDS thioiredoxin H.

SOURCE Triticum aestivum (bread wheat)

ORGANISM Triticum aestivum

REFERENCE 1 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.

AUTHORS Serrato,A.J., Crespo,J.L., Florencio,F.J. and Cejudo,F.J.

TITLE Characterization of two thioiredoxins h with predominant localization in the nucleus of aleurone and scutellum cells of germinating wheat seeds

JOURNAL Plant Mol. Biol. 46 (3), 361-371 (2001)

REFERENCE 2 (bases 1 to 596)

AUTHORS Cejudo,F.J.

TITLE Direct Submission

JOURNAL Submitted (24-JUL-1998) Cejudo F.J., Instituto de Bioquímica Vegetal y Fotosíntesis, Universidad de Sevilla y CSIC, Avda Americo Vespucio s/n, 41092-Sevilla, SPAIN

FEATURES

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QY 43 GGCGGCGAGGAGGTCGCGTGTGTCGCGTGCACACCAAGGACGAGTTTCGACGCCCGCAT 102

Db 97 GCGGTCGGGGCGGGGAGGTGATCTCCGTCACACCTGGACAGTGGACCATGAGAT 146  
Qy 103 GCGCAAGGCCAAGAGCAGGCGAAGCTGGTGGTGCATCGACTTCATGCGCCCGCCGCGTGCAG 162  
Db 147 CGAGGAGGCCAAGCGCCGCAAGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 206  
Qy 163 TGGGTGCGATGATGCGCCCGGTGTCAGCGGACTGCGCCAGCAGTACCTTCCCGGT 222  
Db 207 ACCATGCGGATCATGCTCGCTTCGCTGATCTGCGCCAGAGTTCGCCAATCTGT 266  
Qy 223 CTCTCTCGAGTCGACGTCGACGCAACTGCTGGAAGTTCGCGAAGATCTAGCGGCTCCATGT 282  
Db 267 TTCTCTCAAGTTCGATGCTGATGACTGAGCCCATGCGGAGCAATTCAGCGTTGAGGC 326  
Qy 283 GATCGCACTTCTGCTTCATCAGGACGCGGAGACGCTGAGAGCTTGTCTACCTCGA 342  
Db 327 CATGCCAACCTTCTGCTTCATTAAGGAAGGAGATGTCAGGACAGGTTGTGGAGCTAT 386  
Qy 343 CGAGGACGAGTCCGGGACCGCTGAGGAAGTACGCGCGCGC 384  
Db 387 CAAGGAGGACTGACGAGCAAGTGTGGCTACACGCGCGCGC 428

RESULT 14  
G71188/c 371 bp DNA linear STS 08-JUN-2001  
DEFINITION V0228311FM017 maize leaf DNA Zea mays STS genomic, sequence tagged site.  
ACCESSION G71188  
VERSION G71188.1 GI:14332873  
KEYWORDS STS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 371)  
Yang, Y.J., Guo, L., Ashlock, D.A., Wen, T.J. and Schnable, P.S.  
3' UTR sequences of maize genes  
Unpublished (2001)

Contact: Schnable, P.S.  
Schnable Laboratory  
Iowa State University  
G405 Agronomy Hall, Ames, IA 50011, USA  
Tel: 515-294-0975  
Fax: 515-294-2299  
Email: schnable@iastate.edu  
Primer A: GCAAGCTGGTGGTCATTG  
Primer B: AAGTATCCATGGTTAAGTATCGCC  
PCR Profile:  
Denaturation: 94 degrees C for 30 seconds  
Annealing: 60 degrees C for 45 seconds  
Polymerization: 72 degrees C for 90 seconds  
PCR cycles: 31  
Thermal cycler: Perkin Elmer TC  
Protocol:  
Template: 10-20 ng  
Primer: each 0.5 uM  
dNTPs: each 200 uM  
Taq Polymerase: 0.05 units/ul  
Total vol: 20 ul

Buffer:  
MgCl2: 2 mM  
KCl: 50 mM  
Tris-HCl: 20 mM  
pH: 8.4.  
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FEATURES  
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Qy 213 CTGCTGTCAGTGGGTGCGCAGATGATGCGCCCGGTGTACGCGGACTGCGCCAGCAAGTACC 272  
Db 310 CTGCTGTCAGTGGGTGCGCAGATGATGCGCCCGGTGTACGCGGACTGCGCCAGCAAGTACC 251  
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Db 250 AGTTCGAGGCGATGCGGACCTTCTGCTTCATCAGGACGCGGAGACCTCTCGAGAGCTTTG 191  
Qy 333 CTACCGTCGAGGAGCAGCTCGGACGCGGAGACCTCTCGAGAGCTTTG 392  
Db 190 TGGGTGCGCAGGAGCAGCTCGGACGCGGAGACCTCTCGAGAGCTTTG 131  
Qy 393 CGAGCGCTCTGCTGCT 407  
Db 130 CGTCTGCGTCTGCT 116

RESULT 15  
A48516 393 bp DNA linear PAT 07-MAR-1997  
DEFINITION Sequence 4 from Patent WO9603505.  
ACCESSION A48516  
VERSION A48516.1 GI:2302293  
KEYWORDS Triticum turgidum subsp. durum (durum wheat)  
SOURCE Triticum turgidum subsp. durum  
ORGANISM Triticum turgidum subsp. durum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.  
1 (bases 1 to 393)  
Gauthier, M., Mullien-Pellerin, V., De, L.F. and Joudrier, P.  
HARD AND SOFT WHEAT THIOREDOXINS b, HOMOLOGOUS PROTEINS, DNA FRAGMENTS CODING FOR SAID PROTEINS AND METHODS FOR PREPARING SAME  
Patent: WO 9603505-A 4 08-FEB-1996;  
AGRONOMIQUE INST NAT RECH (FR)  
Other publication AU 3082795 960222  
Other publication FR 2723097 960202.  
Location/Qualifiers  
1..393  
/organism="Triticum turgidum subsp. durum"  
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ORIGIN  
Query Match 17.1%; Score 119.6; DB 6; Length 393;  
Best Local Similarity 59.4%; Pred. No. 1.3e-09;  
Matches 203; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

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QY	103	GGCCAAAGGCCAAGGACAGGGCAGCTGGTGCATCGACTTCATGCCCCCTGGTGCAG	162
Db	108	CGAGGAGGCCAACGCCCGCCCAAGAGCTGGTGGTGAATTGACTTCACTGCATCATGGTGC	167
QY	163	TGGGTGCCAGATCATGGCCCCCGGTGTACCGGACTCGCCAGCAAGTACCTTCCCGGT	222
Db	168	ACCATGCCGATCATGGCTCCAAATTTTGTGATCTCGCCAAAGAGTTCCAGCTGTGT	227
QY	223	CTTCTCGAGGTCGACGTGACGAACTGCTGGAAGTCCGGAAGATCTACGGTCCATGT	282
Db	228	TTTCTCTCAAGGTCGACGTTGATGAAGCCCAATTGCTGAGCAATTGAGGTGAGGC	287
QY	283	GATGCCGACCTTCTGCTTCATCAGGAAACGCGAGACGCTCGAGAGCTTTGCTACCGTCA	342
Db	288	CATGCCAACCTTCTCTGTTGATGAGGAGGAGACGTCAGGACAGGTTGTGGAGCTAT	347
QY	343	CGAGGACGAGCTCCGGGACGCCGTCAGGAAGTACGCCGCCG	384
Db	348	CAAGGAGGAGCTGACGACCAAGGTTGGGCTCCACGGGGTGC	389

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 Job time : 2851.79 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 5, 2004, 19:52:33 ; Search time 2102.06 Seconds  
(without alignments)  
9944.292 Million cell updates/sec

Title: US-10-005-429-13

Perfect score: 700

Sequence: 1 ggaaccacacggaggaag.....aaaaaaaaaaaaaaaaaaaaa 700

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:

1: em\_estba.\*

2: em\_esthum.\*

3: em\_estin.\*

4: em\_estmu.\*

5: em\_estov.\*

6: em\_estpl.\*

7: em\_estro.\*

8: em\_hic.\*

9: gb\_est1.\*

10: gb\_est2.\*

11: gb\_est3.\*

12: gb\_est4.\*

13: gb\_est5.\*

14: gb\_est6.\*

15: em\_estfun.\*

16: em\_estom.\*

17: em\_gss\_hum.\*

18: em\_gss\_inv.\*

19: em\_gss\_pln.\*

20: em\_gss\_vrt.\*

21: em\_gss\_fun.\*

22: em\_gss\_mam.\*

23: em\_gss\_mus.\*

24: em\_gss\_pro.\*

25: em\_gss\_rtd.\*

26: em\_gss\_phg.\*

27: em\_gss\_vrl.\*

28: gb\_gss1.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	502	71.7	562	14	CF005608 QB113b03.
2	497.6	71.1	568	14	CF020146 QB2b06.x
3	474.2	67.7	573	14	CF006552 QB120e10.
4	458.4	65.5	503	14	CF019426 QB19c09.

C	5	457.8	65.4	504	14	CF019475	QB019475
	6	452.4	64.6	496	14	CF007924	QB019475
	7	452.2	64.6	503	14	CF019553	QB15a01.x
	8	447	63.9	480	14	CD978907	QAF6f04.y
	9	411	58.7	430	14	CD972346	QAE320e03.
C	10	408	58.3	442	14	CD974597	QAE48b02.
	11	393	56.1	411	14	CD976888	QAE723b09.
	12	385.8	55.1	427	14	CF647253	CF647253 3530_1_41
C	13	380.4	54.3	400	14	CD974844	QAE50C02.
C	14	379	54.1	388	12	BG837010	BG837010 2m08_10f0
C	15	376.6	53.8	426	14	CF008093	CF017d05.x
C	16	361.8	51.7	859	29	CG158805	QBFVV10TB
C	17	361.8	51.7	887	28	CC402188	PUFV10TB
C	18	361.8	51.7	953	29	CG323449	CG402188
C	19	361.2	51.6	370	14	CF006994	CG3223449
C	20	344	49.1	737	14	CF006844	CG3223449
C	21	339.4	48.5	456	12	BG837151	CG3223449
C	22	337.8	48.3	359	14	CF008092	CG3223449
	23	243	34.7	658	14	CA277200	CG3223449
	24	243	34.7	1056	14	CA275558	CG3223449
	25	233	33.3	519	14	CA273890	CG3223449
C	26	228.8	32.7	273	14	CD965475	CG3223449
C	27	225.8	32.3	316	14	CD949589	CG3223449
C	28	222.2	31.7	673	14	CA275630	CG3223449
C	29	217.8	31.1	681	28	BZ794456	CG3223449
C	30	207.2	29.6	600	14	CF041938	CG3223449
C	31	206.4	29.5	559	14	CD999290	CG3223449
C	32	206.2	29.5	544	9	AI621726	CG3223449
C	33	205.6	29.4	424	12	BI542528	CG3223449
C	34	205.6	29.4	459	14	CD651418	CG3223449
C	35	205.6	29.4	504	14	CF014883	CG3223449
	36	205.6	29.4	513	14	CD996841	CG3223449
	37	205.6	29.4	519	14	CD995652	CG3223449
	38	205.6	29.4	523	14	CF042094	CG3223449
	39	205.6	29.4	550	14	CF023788	CG3223449
C	40	205.6	29.4	553	9	AI438566	CG3223449
	41	205.6	29.4	556	14	CD990879	CG3223449
C	42	205.6	29.4	560	9	AI621711	CG3223449
C	43	205.6	29.4	564	14	CB833972	CG3223449
C	44	205.6	29.4	564	14	CB885343	CG3223449
C	45	205.6	29.4	568	12	BM380699	CG3223449

## ALIGNMENTS

RESULT 1  
CF005608  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

CF005608  
QB113b03.xg  
QB1 Zea mays  
CF005608.1  
GI:32865926  
EST.  
Zea mays  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 562)  
Genoplane.  
Genoplane, a major partnership french program in plant genomics  
Unpublished (2003)  
Contact: Genoplane  
Genoplane  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10

562 bp mRNA linear EST 16-JUL-2003  
cDNA clone QB113b03, mRNA sequence.

FEATUES  
source  
1. 562  
/organism="Zea mays"

This sequence has been generated in the framework of the french plant genomics programme 'Genoplane' (<http://www.genoplane.com>) and <http://genoplane-info.infobiogen.fr>.







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1. .480
   /organism="Zea mays"
   /mol_type="mRNA"
   /cultivar="P2"
   /db_xref="taxon:4577"
   /clone="QAtsf04"
   /tissue_type="pericarp"
   /clone_id="QAt"

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Query Match	63.9%;	Score 447;	DB 14;	Length 480;
Best Local Similarity	99.1%;	Pred. No. 8.4e-41;		
Matches 461;	Conservative 0;	Mismatches 0;	Indels 4;	Gaps 1;
54	AGGGTCCCGTGNATCGGTGCCACACCGAGGAGGAGTTCCAGCCGCCCGCATGGCCAAAGGCCA	113		
1	AGGGTCCCGTGNATCGGTGCCACACCGAGGAGGAGTTCCAGCCGCCCGCATGGCCAAAGGCCA	60		
114	AGGACGAGGCGAAGCTGGTGGTTCATCGAC-----TTTCATGGCCCCCTGGTGCAATGGGTGC	169		
61	AGGACGAGGCGAAGCTGGTGGTTCATCGACTTCTGTTTCATGGCCCCCTGGTGCAATGGGTGC	120		
170	CAGATGATGGCCCCCGGTGTACGGGAGCTGGCCAGCAAGTACCCCTTCGGCGGTCTTCCCTC	229		
121	CAGATGATGGCCCCCGGTGTACGGGAGCTGGCCAGCAAGTACCCCTTCGGCGGTCTTCCCTC	180		
230	GAGGTTCGACGTCCAGCGAACTGCTGGAAGTCCGGAAGATCTACGGCGTCCATGTGATGCCG	289		
181	GAGGTTCGACGTCCAGCGAACTGCTGGAAGTCCGGAAGATCTACGGCGTCCATGTGATGCCG	240		
290	ACCTTCTCGTTCATCAGGAACCGCGAGAGCGCTCGAGAGCTTTGCTACCGTCCGACGAGAC	349		
241	ACCTTCTCGTTCATCAGGAACCGCGAGAGCGCTCGAGAGCTTTGCTACCGTCCGACGAGAC	300		
350	GAGCTCCGGGACGCCGTACGGAAGTACCGCGCGCTGGGCACTACGACGGCTCCTCGCCTCG	409		
301	GAGCTCCGGGACGCCGTACGGAAGTACCGCGCGCTGGGCACTACGACGGCTCCTCGCCTCG	360		
410	GGGTCCGCCTTAATTCAGGAGATGTGATGTGTAGCAAAATAGCGCGCGCGCACCAAGTCGTCA	469		
361	GGGTCCGCCTTAATTCAGGAGATGTGATGTGTAGCAAAATAGCGCGCGCGCACCAAGTCGTCA	420		
470	ATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	514		
421	ATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	465		

CD972346	CD972346	430 bp	mRNA	linear	EST 16-JUL-2003
LOCUS	QAE320e03.yg	QAE	Zea mays	cdna clone	QAE20e03, mRNA sequence.
DEFINITION	CD972346				
ACCESSION	CD972346				
VERSION	CD972346.1	GI:32832668			
KEYWORDS	EST.				
SOURCE	Zea mays				
ORGANISM	Zea mays				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				
REFERENCE	1 (bases 1 to 430)				
AUTHORS	Genoplante.				
TITLE	Genoplante. a major partnership french program in plant genomics				

JOURNAL  
COMMENT

Unpublished (2003)  
Contact: Genoplatte  
Genoplatte  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>  
and <http://genoplatte-info.inbioigen.fr/>).

FEATURES  
source

Location/Qualifiers  
1. 430  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="P2"  
/db\_xref="taxon:4577"  
/clone="QAE20e03"  
/tissue\_type="pericarp"  
/clone\_lib="QAE"

ORIGIN

Query Match 58.7%; Score 411; DB 14; Length 430;  
Best Local Similarity 99.1%; Pred. No. 8.7e-37;  
Matches 425; Conservative 0; Mismatches 0; Indels 4; Gaps 1;  
QY 54 AGGTCGCGTGATCGGTGTCACACCAAGGACGAGTTGCAAGCCCGCATGGCCAGGCCA 113  
DB 1 AGGTCGCGTGATCGGTGTCACACCAAGGACGAGTTGCAAGCCCGCATGGCCAGGCCA 60  
QY 114 AGGACAGGCGAAGCTGGTGTGATCGAC-----TTATCGCCCGCTGTCAGTGGGTGC 169  
DB 61 AGGACAGGCGAAGCTGGTGTGATCGAC-----TTATCGCCCGCTGTCAGTGGGTGC 120  
QY 170 CAGATGATGCGCCCGGTGTACGGGAGCTGCGCAGCAAGTACCCCTTCGCGGCTTCCTTC 229  
DB 121 CAGATGATGCGCCCGGTGTACGGGAGCTGCGCAGCAAGTACCCCTTCGCGGCTTCCTTC 180  
QY 230 GAGTGCACTCGAAGCACTGCTGGAAGTCCGCAAGATCTACGGCTCCATGTGATCCCG 289  
DB 181 GAGTGCACTCGAAGCACTGCTGGAAGTCCGCAAGATCTACGGCTCCATGTGATCCCG 240  
QY 290 ACCTTCGCTTCATCAGGAACGCGAGACGCTCGAGAGCTTTCGTACCGTCGACGAGGAC 349  
DB 241 ACCTTCGCTTCATCAGGAACGCGAGACGCTCGAGAGCTTTCGTACCGTCGACGAGGAC 300  
QY 350 GAGTCGCGGACGCGTCAGGAAGTACGCGCGCTGCGCACTACGAGGCTTCGCTCG 409  
DB 301 GAGTCGCGGACGCGTCAGGAAGTACGCGCGCTGCGCACTACGAGGCTTCGCTCG 360  
QY 410 GCGTCGCGCTTAATTCAGGATGTGTGTAGCAATACGCGCGGCGACCACTGCTCA 469  
DB 361 GCGTCGCGCTTAATTCAGGATGTGTGTAGCAATACGCGCGGCGACCACTGCTCA 420  
QY 470 ATAAATAAA 478  
DB 421 ATAAATAAA 429

RESULT 10  
CD974597/c

LOCUS  
DEFINITION  
QAE48b02.yg QAE Zea mays cDNA clone QAE48b02, mRNA sequence.  
ACCESSION  
CD974597  
VERSION  
CD974597.1 GI:32834919  
KEYWORDS  
EST.  
SOURCE  
Zea mays  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 442)  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Unpublished (2003)

COMMENT

Contact: Genoplatte  
Genoplatte  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>  
and <http://genoplatte-info.inbioigen.fr/>).

FEATURES  
source

Location/Qualifiers  
1. 442  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="P2"  
/db\_xref="taxon:4577"  
/clone="QAE48b02"  
/tissue\_type="pericarp"  
/clone\_lib="QAE"

ORIGIN

Query Match 58.3%; Score 408; DB 14; Length 442;  
Best Local Similarity 97.9%; Pred. No. 1.8e-36;  
Matches 425; Conservative 0; Mismatches 5; Indels 4; Gaps 1;  
QY 42 TGGCGCGGAGGAGGTCGCGTGATCGGTGTCACACCAAGGACGAGTTGCAAGCCCGCA 101  
DB 434 TGGCGCGGAGGAGGTCGCGTGATCGGTGTCACACCAAGGACGAGTTGCAAGCCCGCA 375  
QY 102 TGGCAAGGCCAAGAGCAGGCAAGCTGGTGTGATCGAC-----TTCATGGCCCCCTGG 157  
DB 374 TGGCAAGGCCAAGAGCAGGCAAGCTGGTGTGATCGAC-----TTCATGGCCCCCTGG 315  
QY 158 TCGAGTGGGTGTCAGATGATGCGCCCGGTGACGGGAGCTGCGCAGCAAGTACCTTCC 217  
DB 314 TCGAGTGGGTGTCAGATGATGCGCCCGGTGACGGGAGCTGCGCAGCAAGTACCTTCC 255  
QY 218 GCGGCTCTCTCTCGAGGTGCAAGCTCGAAGTCTGCTGGAAGTCCGGAAGATCTACGGCGTC 277  
DB 254 GCGGCTCTCTCTCGAGGTGCAAGCTCGAAGTCTGCTGGAAGTCCGGAAGATCTACGGCGTC 195  
QY 278 CATGTGATCGCACTCTCTCTGCTTCATCAGACCGCGGAGCGCTCGAGAGCTTGTCTACC 337  
DB 194 CATGTGATCGCACTCTCTGCTTCATCAGAAACCGGAGCGCTCGAGAGCTTGTCTACC 135  
QY 338 GTCGACGAGGAGAGCTCGCGGACGCGCTCAGAAAGTACCGCGCGCTGGCACTACGAG 397  
DB 134 GTCGACGAGGAGAGCTCGCGGACGCGCTCAGAAAGTACCGCGCGCTGGCACTACGAG 75  
QY 398 GTCCTGCTCGGCTCGCGCTTAATTCAGGATGTGTGTAGCAATACGCGCGCG 457  
DB 74 GTCCTGCTCGGCTCGCGCTTAATTCAGGATGTGTGTAGCAATACGCGCGCG 15  
QY 458 CACCACTGCTCAAT 471  
DB 14 CACCACTGCTCAAT 1

RESULT 11  
CD976888

LOCUS  
DEFINITION  
QAF23b09.yg QAF Zea mays cDNA clone QAF23b09, mRNA sequence.  
ACCESSION  
CD976888  
VERSION  
CD976888.1 GI:32837210  
KEYWORDS  
EST.  
SOURCE  
Zea mays  
ORGANISM  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 411)  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
Unpublished (2003)  
Contact: Genoplatte

Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>)  
and <http://genoplante-info.infobiogen.fr>.

FEATURES

source  
1. 411  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="P2"  
/db\_xref="taxon:4577"  
/clone="QAF23b09"  
/tissue\_type="pericarp"  
/clone\_lib="QAF"

ORIGIN

Query Match 56.1%; Score 393; DB 14; Length 411;  
Best Local Similarity 99.0%; Pred. No. 8.8e-35;  
Matches 407; Conservative 0; Mismatches 0; Indels 4; Gaps 1;  
Qy 54 AGGTGCGGTGATCGGTGCGCACCAAGGACGAGTTGCGACGCCCGCATGGCCCAAGGCCA 113  
Db 1 AGGTGCGGTGATCGGTGCGCACCAAGGACGAGTTGCGACGCCCGCATGGCCCAAGGCCA 60  
Qy 114 AGGAGCAGGCGAGCTGTGTCTATCCAC---TTCTATGCGCCCTGTGCGATGGTGGTC 169  
Db 61 AGGAGCAGGCGAGCTGTGTCTATCCAC---TTCTATGCGCCCTGTGCGATGGTGGTC 120  
Qy 170 CAGATGATGCGCCCGGTGTACGGGAGCTGCGGACGAGTACCTTTCCGGGTCTTCTC 229  
Db 121 CAGATGATGCGCCCGGTGTACGGGAGCTGCGGACGAGTACCTTTCCGGGTCTTCTC 180  
Qy 230 GAGTTCACGTCGACGAGTCTGGAAGTCGCGAGTCTACGCGCTTCCGCGGTCTTCTC 289  
Db 181 GAGTTCACGTCGACGAGTCTGGAAGTCGCGAGTCTACGCGCTTCCGCGGTCTTCTC 240  
Qy 290 ACCTTCGTCTCATCAGGAACGCGAGACCTCTGAGAGCTTTTCTACCTCGACGAGGAC 349  
Db 241 ACCTTCGTCTCATCAGGAACGCGAGACCTCTGAGAGCTTTTCTACCTCGACGAGGAC 300  
Qy 350 GAGTTCGCGGACGCGTCAGGAGTACGCGCGCTGCGACGAGTACGCGCTTCCGCGGTCTTCTC 409  
Db 301 GAGTTCGCGGACGCGTCAGGAGTACGCGCGCTGCGACGAGTACGCGCTTCCGCGGTCTTCTC 360  
Qy 410 GGTTCGCGCTTAATTCAGGAGATGTGTGTAGCAAAATAGCGCGCGCAC 460  
Db 361 GGTTCGCGCTTAATTCAGGAGATGTGTGTAGCAAAATAGCGCGCGCAC 411

RESULT 12

CF647253  
LOCUS 427 bp mRNA linear EST 02-OCT-2003  
DEFINITION 3530.1\_41.1\_D03.x.1\_3530 - Full length cDNA library created by  
Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.  
CF647253  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Zea mays

REFERENCE

AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 427)  
Walbot, V.  
Maize ESTs from various cDNA libraries sequenced at Stanford  
University  
Unpublished (1999)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227  
Fax: 650 725 8221  
Email: [walbot@stanford.edu](mailto:walbot@stanford.edu)  
Plate: 3530.1\_41.1 row: D column: 03.

FEATURES

source  
1. 427  
/organism="Zea mays"  
/mol\_type="mRNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/tissue\_type="multiple"  
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/lab\_host="DH10B"

/clone\_lib="3530 - Full length cDNA library created by  
Invitrogen from multiple tissues"  
/note="Organ: silks, husks, ears, pollen, shoot tips,  
leaf, root tips, whole seed, embryo; Vector: pCMV-SPORT  
6.1; Site 1: EcoRV; Site 2: NotI; Maize Gene Discovery  
Project contracted with Invitrogen to produce a  
normalized, full length library in a pSPORT vector. This  
is a Gateway compatible vector, permitting clone movement  
to new vector backbones for expression in diverse host  
cells using recombination rather than restriction enzymes.  
Details of the vector and sequencing primers are available  
at ZmDB in the EST library description tables. poly(A)+  
mRNA was prepared by Invitrogen, and equimolar amounts of  
RNA from each of the 12 tissue samples were mixed together  
for selection of mRNA with a 5' cap. After synthesis of  
cDNA, a normalization step was conducted against the  
mixture of RNA sources. This step effected a 20X to 80X  
reduction in common transcript types. Tissues prepared: 1.  
just emerging silks; 2. inner husks from ears of sample  
#1; 3. 20 day aleurone; 4. immature tassels, stages from  
1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm  
vegetative shoot tips from 15 day old seedlings; all  
leaves with an expanded or partially expanded sheath  
were removed; 8. mature leaf tissue; 9. 0.5 cm long root  
tips from 15 day old seedlings; 10. 10 day whole seed; 11.  
12 day endosperm and embryo; 12. 17 day endosperm and  
embryo. All of the sequenced clones in project 3530 will  
be archived at the University of Arizona along with the  
unigene clones from the Maize Gene Discovery EST  
sequencing projects. Clones can be ordered through the  
ZmDB web site or directly from the University of Arizona  
(<http://www.genome.arizona.edu/orders/>). High density  
filters containing over 18,000 clones can also be ordered  
from the University of Arizona."

ORIGIN

Query Match 55.1%; Score 385.8; DB 14; Length 427;  
Best Local Similarity 98.3%; Pred. No. 5.4e-34;  
Matches 401; Conservative 0; Mismatches 3; Indels 4; Gaps 1;  
Qy 1 GGATCCACACCCGAGGAAGGAGAAGA---GAGGGTCCGAATAATGCGCGGAGGAGG 56  
Db 20 GGATCCACACCCGAGGAAGGAGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 79  
Qy 57 GTGCGCGTATCGGTGCGCACCAAGGAGAGTTCACGCCCGCATGGCCCAAGGCCAAG 116  
Db 80 GTGCGCGTATCGGTGCGCACCAAGGAGAGTTCACGCCCGCATGGCCCAAGGCCAAG 139  
Qy 117 AGCAGGCGAAGCTGTGGTTCATCGATTTCATGCCCGCCCTGGTGCAGTGGTCCAGATCA 176  
Db 140 AGCAGGCGAAGCTGTGGTTCATCGATTTCATGCCCGCCCTGGTGCAGTGGTCCAGATCA 199  
Qy 177 TGGCCCCGGGTACGCGGACTGCGCGCAGCAAGTACCTTCCCGGGTCTTCCCTCGAGTGC 236  
Db 200 TGGCCCCGGGTACGCGGACTGCGCGCAGCAAGTACCTTCCCGGGTCTTCCCTCGAGTGC 259  
Qy 237 ACCTGCGAAGAACTGCTGGAGAGTCGCGAAGATCTACGGCGTCCATGTGATGTCGCGACCTTCT 296  
Db 260 ACCTGCGAAGAACTGCTGGAGAGTCGCGAAGATCTACGGCGTCCATGTGATGTCGCGACCTTCT 319

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QY 297 GCTTCATCAGGAACGGGAGAGCTCGAGAGCTTGTCTACCTCGACGAGGACGAGCTCC 356
Db 320 GCTTCATCAGGAACGGGAGAGCTCGAGAGCTTGTCTACCTCGACGAGGACGAGCTCC 379
QY 357 GGGAGCCGCTCAGGAAGTACGCGCGCTGCGACTTACGACGCGCTCTG 404
Db 380 GGGAGCCGCTCAGGAAGTACGCGCGCTGCGACTTACGACGCGCTCTG 427

RESULT 13
LOCUS CD974844/c
DEFINITION QAE50c02.Y9 QAE Zea mays cDNA clone QAE50c02, mRNA sequence.
ACCESSION CD974844
VERSION CD974844.1 GI:32835166
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 400)

AUTHORS
Harris, L.J., Balcerzak, M., Allard, S., Saparno, A., Couroux, P., De
Moors, A., Hattori, J.I., Ouellet, T., Robert, L.S., Singh, J.A.,
Spott, D. and Tinker, N.A.
TITLE Expressed Sequence Tags from Developing Maize Kernels Six Days
after Silk Channel Inoculation with Fusarium graminearum
JOURNAL Unpublished (2003)
COMMENT Contact: Genoplatte
Genoplatte
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genoplatte' (http://www.genoplatte.com)
and http://genoplatte-info.infobiogen.fr.

FEATURES
Location/Qualifiers
1..400
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="F2"
/db_xref="taxon:4577"
/clone="QAE50c02"
/tissue_type="pericarp"
/clone_lib="QAE"

ORIGIN
Query Match 54.3%; Score 380.4; DB 14; Length 400;
Best Local Similarity 98.8%; Pred. No. 2.2e-33;
Matches 395; Conservative 0; Mismatches 1; Indels 4; Gaps 1;

QY 76 CACCAAGACGAGTTCGACGCGCGCATGCCAAGGCCAAGGAGCAGGCGAGCTGGT 135
Db 400 CACCAAGACGAGTTCGACGCGCGCATGCCAAGGCCAAGGAGCAGGCGAGCTGGT 341

QY 136 CATCGAC-----TTATGCGCCCGCTGGTGCATGGTGCAGATGATGCGCCCGGTGACG 191
Db 340 CATCGACTTCGTTCTATGCGCCCGCTGGTGCATGGTGCAGATGATGCGCCCGGTGACG 281

QY 192 CGGACTCGCGCAGCAAGTACCTTCGCGGCTTCCTCGAGTGCAGTGCAGCACTGC 251
Db 280 CGGACTCGCGCAGCAAGTACCTTCGCGGCTTCCTCGAGTGCAGTGCAGCACTGC 221

QY 252 TGGAGTGCAGGAATCTACGGGTTCATGTGATGCCGACCTTCTGTTTCATCAGGAACG 311
Db 220 TGGAGTGCAGGAATCTACGGGTTCATGTGATGCCGACCTTCTGTTTCATCAGGAACG 161

QY 312 GGGAGACGCTCGAGAGCTTTGTCTACCTCGCAGGAGCAGCTCCGGGACGCGTCAAG 371
Db 160 GGGAGACGCTCGAGAGCTTTGTCTACCTCGCAGGAGCAGCTCCGGGACGCGTCAAG 101

QY 372 AGTACGCGCGCTGGCACTACGAGGCTCTGCTCGGCTTCGCTTAATTCAGGAGAT 431
Db 100 AGTACGCGCGCTGGCACTACGAGGCTCTGCTCGGCTTCGCTTAATTCAGGAGAT 41

QY 432 GTGATGTGTAGCAATAGCGCGCGCAGCTCGTCAAT 471

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Db 40 GTGATGTGTAGCAATAGCGCGCGCAGCTCGTCAAT 1

RESULT 14
LOCUS BG837010/c
DEFINITION BG837010.1 GI:14203333
ACCESSION BG837010
VERSION BG837010.1
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 388)

AUTHORS
Harris, L.J., Balcerzak, M., Allard, S., Saparno, A., Couroux, P., De
Moors, A., Hattori, J.I., Ouellet, T., Robert, L.S., Singh, J.A.,
Spott, D. and Tinker, N.A.
TITLE Expressed Sequence Tags from Developing Maize Kernels Six Days
after Silk Channel Inoculation with Fusarium graminearum
JOURNAL Unpublished (2001)
COMMENT Contact: Harris, Linda J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 21, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,
CANADA
Tel: (613) 759-1314
Fax: (613) 759-6566
Email: harrisjl@em.agr.ca.

FEATURES
Location/Qualifiers
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/organism="Zea mays"
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/cultivar="CO430"
/db_xref="taxon:4577"
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/clone_lib="Zm08_AAPC_ECORC_Fusarium_graminearum_inoculate
d_corn_ear"
/notes="Vector: Bluescript SK+/XhoI-EcoRI; Site 1: EcoRI;
Site 2: XhoI; Field-grown maize ears were silk
channel-inoculated in the morning (~10 am) with 1 ml of a
Fusarium graminearum macroconidial suspension (500,000
spores/ml) and whole ears were collected and immediately
frozen in liquid nitrogen 6 days later."

ORIGIN
Query Match 54.1%; Score 379; DB 12; Length 388;
Best Local Similarity 98.7%; Pred. No. 3.2e-33;
Matches 382; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 62 GTGATCGGTGCGACCAAGGAGTTCGACGCGCGCATGGCCAGGCCAAGGAGCAG 121
Db 387 GTGATCGGTGCGACCAAGGAGTTCGACGCGCGCATGGCCAGGCCAAGGAGCAG 328

QY 122 GCGAAGCTGGTGGTGCATCGACTTCATGCGCCCTTCGTCGATGGTGCAGATGATGCC 181
Db 327 GCGAAGCTGGTGGTGCATCGACTTCATGCGCCCTTCGTCGATGGTGCAGATGATGCC 268

QY 182 CGGCTGTACGCGGACTGCGCCAGGAGTACCTTCGCGGCTTCCTCGAGTGCAGCTC 241
Db 267 CGGCTGTACGCGGACTGCGCCAGGAGTACCTTCGCGGCTTCCTCGAGTGCAGCTC 208

QY 242 GACGAACCTGCTGGAAAGTCGGAAGATCTACGGGTCGATGTGATGCCAGCTTCGCTTC 301
Db 207 GACGAACCTGCTGGAAAGTCGGAAGATCTACGGGTCGATGTGATGCCAGCTTCGCTTC 148

QY 302 ATCAGGAACGGCGAGCGCTCGAGAGCTTTGCTACCTCGTCCGACGAGGAGCTCCGGAC 361

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[illegible]

RESULT 15	CF008093	CF008093	426 bp	mRNA	linear	EST 16-JUL-2003
LOCUS	QBI7405.xg	QBI Zea mays cDNA clone QBI7d05,				mrna sequence.
DEFINITION	CF008093					
ACCESSION	CF008093.1	GI:32868411				
VERSION	EST.					
KEYWORDS						
SOURCE	Zea mays					
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.					
REFERENCE	1 (bases 1 to 426)					
AUTHORS	Genopante.					
TITLE	Genopante, a major partnership french program in plant genomics					
JOURNAL	Unpublished (2003)					
COMMENT	Contact: Genopante					
	Genopante					
	93, rue Henri Rochefort 91025 EVRY CEDEX France					
	Tel: 33 1 69 47 54 00					
	Fax: 33 1 69 47 54 10					
	This sequence has been generated in the framework of the french plant genomics programme 'Genopante' ( <a href="http://www.genopante.com">http://www.genopante.com</a> and <a href="http://genopante-info.infobiogen.fr">http://genopante-info.infobiogen.fr</a> ).					

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    /clone_lib="OB1"

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Best Local Similarity	98.0%	Pred. No.	5.7e-33				
Matches	393	Conservative	0	Mismatches	4	Indels	4
Gaps	1						

  

QY	1	GGATCCACACCGAGGAAAGAGAGAGAGGGTCGGATAATATGCGCGCCGAGGAGGGTGC	60
Db	26	GGATCCACACCGAGGAAAGAGAGAGAGGGTCGGATAATGTCGCCCGAGGAGGGTGC	85
QY	61	CGTGATCGCGTGCACACCAAGAGAGAGTTTCEAGCCCGCGCATGCCCAAGGCCCAAGAGGCA	120
Db	86	CGTGATCGCGTGCACACCAAGAGAGAGTTTCEAGCCCGCGCATGCCCAAGGCCCAAGAGGCA	145
QY	121	GGGCAAGCTGGTGGTCAATCGACT---TCATGGCCCCCTGGTGCAGTGGGTGCCAGATGA	176
Db	146	GGGCAAGCTGGTGGTCAATCGACTTCGGTCAATGGCCCCCTGGTGCAGTGGGTGCCAGATGA	205
QY	177	TGGCCCCGGTGATACCGGAGCTGCGCCAGCAAGTACCCCTTCCGCGGTCTTCTTCGAGGTGC	236
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QY	237	ACGTCGACGACTGCTGGAAGTCCGAGATCTACGGCGTCCATGTGATGCCGACCTTCT	296
Db	266	ACGTCGACGACTGCTGGAAGTCCGGAAGATCTACGGCGTCCATGTGATGCCGACCTTCT	325
QY	297	GCTTTCATCAGGAACGGCGAGACGCTTCGAGAGCTTTGGTTACCGTCCAGCGAGGACGAGCTCC	356

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 5, 2004, 19:42:32 ; Search time 58.7917 Seconds  
(without alignments)  
6607.485 Million cell updates/sec

Title: US-10-005-429-13  
Perfect score: 700  
Sequence: 1 ggatccacacaggagaaag.....aaaaaaaaaaaaaaaaaaaaa 700

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
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2: /cgn2\_6/prodata/2/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/prodata/2/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/prodata/2/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/prodata/2/ina/6C\_COMB.seq.\*  
6: /cgn2\_6/prodata/2/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	195.2	27.9	466	4	US-09-621-976-1844
2	137.2	19.6	318	4	US-09-313-294A-5868
3	120	17.1	382	4	US-09-540-014-3
4	119.6	17.1	393	4	US-09-540-014-5
5	111.8	16.9	369	4	US-09-540-014-1
6	113.6	16.2	278	4	US-09-313-294A-5840
7	87.6	12.5	653	1	US-08-181-271A-103
8	87.6	12.5	653	1	US-08-449-315-103
9	87.6	12.5	653	1	US-08-444-803-103
10	87.6	12.5	653	1	US-08-449-043-103
11	87.6	12.5	653	1	US-08-456-265A-103
12	87.6	12.5	653	1	US-08-455-416-103
13	87.6	12.5	653	1	US-08-455-244-103
14	87.6	12.5	653	1	US-08-454-876-103
15	87.6	12.5	653	2	US-08-457-364-103
16	87.6	12.5	653	2	US-08-456-262-103
17	87.6	12.5	653	2	US-08-456-240-103
18	87.6	12.5	653	2	US-08-455-736-103
19	87.6	12.5	653	2	US-08-971-217-103
20	87.6	12.5	653	3	US-09-350-600-103
21	87.6	12.5	653	4	US-09-306-234-103
22	77.8	11.1	914	1	US-08-386-729A-9
23	72.2	10.3	759	4	US-09-465-559-5
24	71.4	10.2	1872	4	US-09-291-922-27
25	71.4	10.2	1985	4	US-09-907-794A-212
26	71.4	10.2	1985	4	US-09-905-125A-212
27	71.4	10.2	1985	4	US-09-902-775A-212

28	71	10.1	255	4	US-09-621-976-9406	Sequence 9406, Ap
29	71	10.1	1725	4	US-09-668-097A-21	Sequence 21, Appl
30	70.4	10.1	2186	4	US-09-360-545-66	Sequence 66, Appl
c 31	70.4	10.1	10288	4	US-09-845-917A-28	Sequence 28, Appl
c 32	70.4	10.1	13414	4	US-09-845-917A-27	Sequence 27, Appl
33	70.2	10.0	1008	4	US-09-780-641-1	Sequence 1, Appl
34	70	10.0	183	4	US-09-621-976-13606	Sequence 13606, A
35	69.6	9.9	1582	3	US-08-545-196B-10	Sequence 10, Appl
36	69.6	9.9	1582	3	US-08-545-196B-12	Sequence 12, Appl
37	69.2	9.9	2550	6	5258287-23	Patent No. 5258287
38	68.8	9.8	1602	1	US-08-530-950-3	Sequence 3, Appl
39	68.8	9.8	1602	3	US-08-888-429A-3	Sequence 3, Appl
40	68.8	9.8	1602	3	US-09-149-879-3	Sequence 3, Appl
41	68.8	9.8	1602	4	US-09-057-009-3	Sequence 3, Appl
42	68.8	9.8	1602	4	US-09-593-653-3	Sequence 3, Appl
43	68.8	9.8	8100	4	US-09-554-337-4	Sequence 4, Appl
44	68.8	9.8	11517	1	US-07-920-281C-1	Sequence 1, Appl
45	68.8	9.8	11517	3	US-08-466-277-1	Sequence 1, Appl

RESULT 1  
US-09-621-976-1844  
; Sequence 1844, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET 054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 1844  
; LENGTH: 466  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 71..256  
; NAME/KEY: sig\_peptide  
; LOCATION: 71..199  
; OTHER INFORMATION: Von Heijne matrix  
; OTHER INFORMATION: score 4.30000019073486  
; OTHER INFORMATION: seq WVIDFAWCVHA/AP  
US-09-621-976-1844

Query Match 27.9%; Score 195.2; DB 4; Length 466;  
Best Local Similarity 72.0%; Pred. No. 3.3e-31;  
Matches 268; Conservative 0; Mismatches 103; Indels 1; Gaps 1;

QY	36	GAATATGGCGGCGAGGAGGTCGCGTGTGTCGTCACACCAAGGAGGATTCGAGC	95
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Db	126	CCCATATGACCAAGCCCAAGGAGGAGTCGCGTGTGTCACGACCTTCATGGCCCTT	185
QY	156	GTCGAGTGGGTCGAGATGATGTCGCGGTCGCGGAGTCGCGGAGGAGTACCTT	215
Db	186	GCTGTC-GTCCATGCGCGCCATCGCCCACTGTCGCGGAGGAGGATTCACCTC	244
QY	216	CCGCGGTCCTTCCTCGAGGTCGAGGAGTCGCGGAGGAGGATTCACGCGG	275
Db	245	AGTTCGTCCTTCCTCGAGGTCGAGGAGTCGCGGAGGAGGATTCACGCGG	304
QY	276	TCCATGTGATGCGGACCTTTCGCTTCATCGAGGAGGAGGATTCGAGGATTCGTA	335

ALIGNMENTS



Query Match 16.9%; Score 118; DB 4; Length 369;  
Best Local Similarity 59.1%; Pred. No. 1.5e-15;  
Matches 202; Conservative 0; Mismatches 140; Indels 0; Gaps 0;  
QY 43 GCGCGCCGAGGAGGTCCTGATCGCGTCCACCAAGGACGAGTTCCAGCCCGCAT 102  
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QY 103 GCGCAAGCCCAAGAGGAGGCGGAGCTGGTGTGATCATGCTTTCATGCGCCCTGTCGAG 162  
DB 81 CGAGGAGGCCACACACCGCCCAAGAGCTGGTGGTGAITGACTTCACTCATGCTGCTGCGG 140  
QY 163 TGGGTGCAGATGATGCCCGCGGTGTACGGCGACTGCGCCAGCAAGTACCTTCGCGCGT 222  
DB 141 ACCATGCGCATCATGCTCCAGTTTCGCTGATCTCGCCAGAGATTCCCAATGCTGT 200  
QY 223 CTTCCTCGAGGTGACGTGACAGCAACTGCTGGAAGTCCGGAAGTCTACGCGTCCATGT 282  
DB 201 TTTCCTCAAGTCCAGCTGAGTGAATCAAGCCCAATGCTGAGCAATTCAGTGTGAGGC 260  
QY 283 GATCCGCACTTCGCTTCATCAGCAAGCGGAGAGCTCGAGAGCTTGTCTACCGTCA 342  
DB 261 CATCCCAAGTTCCTGTTTCATGAAGAGAGAGCTCAAGCAAGGTTGTCGAGGCTAT 320  
QY 343 CGAGGAGGAGCTCCGCGGAGCGCTCAGGAAGTACGCGCGCGC 384  
DB 321 CAAGGAGGAGCTGACCGCCAGGTTGGGCTTCACGCGCGCGC 362  
RESULT 6  
US-09-313-294A-5840  
; Sequence 5840, Application US/09313294A  
; Patent No. 6476212  
; GENERAL INFORMATION:  
; APPLICANT: Lalgudi, Raghunath V.  
; APPLICANT: Ito, Laura Y.  
; APPLICANT: Sherman, Bradley K.  
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR  
; FILE REFERENCE: PL-0017 US  
; CURRENT APPLICATION NUMBER: US/09/313.294A  
; CURRENT FILING DATE: 1999-05-14  
; NUMBER OF SEQ ID NOS: 7600  
; SOFTWARE: PERL Program  
; SEQ ID NO 5840  
; LENGTH: 278  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURES:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 6476212 700350762H1  
; NAME/KEY: unsure  
; LOCATION: 275  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-313-294A-5840  
Query Match 16.2%; Score 113.6; DB 4; Length 278;  
Best Local Similarity 71.6%; Pred. No. 1.1e-14;  
Matches 149; Conservative 0; Mismatches 59; Indels 0; Gaps 0;  
QY 36 GAATAATGCGCGCGAGGAGGTCGCGGTGATCGGTGTCACCAAGGACGAGTTGACG 95  
DB 41 GATCAATGCGGTCCGAGCAGGAGTCTGTGATCGGTGTCACCAAGGAGTGTGACG 100  
QY 96 CCGCATGCGCCCAAGCCCAAGCAGGAGGTCGCTGATCATGCTTTCATGCGCCCT 155  
DB 101 CCCATGACCAAGGCCCAAGAGCCCGGAGTGGTGTGATCATGCTTTCATGCGCT 160  
QY 156 GGTGAGTGGGTGCGAGATGATGCGCCCGGTGTGATGCGGAGTGTGCGGAGGAGTACCTT 215  
DB 161 GGTGCGTCCATGCGCGCCATGCGCCCATGCTGTTGTTGGAACACGCGCAAGATTTCATTC 220  
QY 216 CCGCGTCTTCTCGAGGTGACGCTCA 243

Query Match 17.1%; Score 119.6; DB 4; Length 393;  
Best Local Similarity 59.4%; Pred. No. 7.4e-16;  
Matches 203; Conservative 0; Mismatches 139; Indels 0; Gaps 0;  
QY 43 GCGCGCCGAGGAGGTCGCGTGCCTGCGCCACCAAGGACGAGTTCCAGCCCGCAT 102  
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QY 103 GCGCAAGCCCAAGAGGAGGCGGAGCTGGTGTGATCATGCTTTCATGCGCCCTGTCGAG 162  
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RESULT 5  
US-09-540-014-1  
; Sequence 1, Application US/09540014  
; Patent No. 6380372  
; GENERAL INFORMATION:  
; APPLICANT: Cho, Myeong-Je  
; APPLICANT: Del Val, Greg  
; APPLICANT: Caillau, Maxime  
; APPLICANT: Lemauz, Peggy G.  
; APPLICANT: Buchanan, Bob B.  
; TITLE OF INVENTION: Barley Gene for Thioredoxin and  
; FILE REFERENCE: NADP-Thioredoxin Reductase  
; CURRENT APPLICATION NUMBER: US/09/540,014  
; CURRENT FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: US 60/127,198  
; PRIOR FILING DATE: 1999-03-31  
; PRIOR APPLICATION NUMBER: US 60/169,162  
; PRIOR FILING DATE: 1999-12-06  
; PRIOR APPLICATION NUMBER: US 60/177,740  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: US 60/177,739  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 369  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: barley thioredoxin h cDNA  
US-09-540-014-1

## RESULT 7

US-08-181-271A-103  
; Sequence 103, Application US/08181271A  
; Patent No. 5614395

## GENERAL INFORMATION:

; APPLICANT: Ryals, John A.  
; APPLICANT: Alexander, Danny C.  
; APPLICANT: Beck, James J.  
; APPLICANT: Duesing, John H.  
; APPLICANT: Friedrich, Leslie B.  
; APPLICANT: Goodman, Robert M.  
; APPLICANT: Harms, Christian  
; APPLICANT: Meins, Jr., Frederick  
; APPLICANT: Montoya, Alice  
; APPLICANT: Moyer, Mary B.  
; APPLICANT: Neuhaus, Jean-Marc  
; APPLICANT: Payne, George B.  
; APPLICANT: Sperison, Christoph  
; APPLICANT: Stinson, Jeffrey R.  
; APPLICANT: Umes, Scott J.  
; APPLICANT: Ward, Eric R.  
; APPLICANT: Williams, Shericca C.

; TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF

; NUMBER OF SEQUENCES: 106

## CORRESPONDENCE ADDRESS:

; ADDRESSEE: CIBA-GEIGY Corporation  
; STREET: 7 Skyline Drive  
; CITY: Hawthorne  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10532

## COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25

## CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/181.271A  
; FILING DATE: 13-JAN-94

## CLASSIFICATION: 435

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/093,301  
; FILING DATE: 16-JUL-1993

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/937,197  
; FILING DATE: 6-NOV-1992

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/678,378  
; FILING DATE: 1-APR-1991

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/305,566  
; FILING DATE: 6-FEB-1989

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/165,667  
; FILING DATE: 8-MAR-1988

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/042,847  
; FILING DATE: 6-APR-1993

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/632,441  
; FILING DATE: 21-DEC-1990

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/425,504  
; FILING DATE: 20-OCT-1989

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/848,506  
; FILING DATE: 6-MAR-1992

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/768,122

; FILING DATE: 27-SEP-1991

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/580,431

; FILING DATE: 7-SEP-1990

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/368,672

; FILING DATE: 20-JUN-1989

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/329,018

; FILING DATE: 24-MAR-1989

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/045,957

; FILING DATE: 12-APR-1993

; ATTORNEY/AGENT INFORMATION:  
; NAME: Elmer, James Scott

; REGISTRATION NUMBER: 36,129

; REFERENCE/DOCKET NUMBER: S-19825/PI/CGC 1727

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8614

; TELEFAX: (919)541-8689

; INFORMATION FOR SEQ ID NO: 103:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 653 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; US-08-181-271A-103

Query Match 12.5%; Score 87.6; DB 1; Length 653;

Best Local Similarity 54.4%; Pred No. 2.7e-09;

Matches 197; Conservative 0; Mismatches 164; Indels 1; Gaps 1;

QY 48 CCGAGGAGGGTCCCGTGAFCGGTCCCAACCAAGACGAGTTCGACGCCCGCATGGCCA 107

Db 73 CCGAGGAGGGACAAAGTGTTCGGCTGCCCAACAGGTTGAGGAATGGAACGAGTACTTCAAGA 132

QY 108 AGCCCAAGCAGCAGGCGGAGCTGCTCATCTGCTTTCATGCCCCCTCGTGGTGGGT 167

Db 133 AAGCGCTTGAGACTAAGAACTGTTGGTGTGATTTTACTGCTTCATGTTGGGSCCTT 192

QY 168 GCCAGATGATGCCCGCGGTGTACGCGGACTGCGCCAGCAAGTACCTTCGCGGGTCTTC 227

Db 193 GCGTTTATTTGCCCAATTCCTGTGACATGCTAAGAGATGCCCATGTTATATTC 252

QY 228 TCGAGTTCAGCTGCGAGCACTGCTGGAAGTCGCG-CAAGATCTACGCGCTCCATGTGATG 286

Db 253 TCAAGGTTGATGTTGATGAACCTGAAGACTGTTTCAGCGGGAATGGAGTGTGGAGGCAATG 312

QY 287 CCGACCTTCTGCTTCATCAGGAACCGCGGAGACGCTCGAGAGCTTTGCTACCGTCGACGAG 346

Db 313 CCAACTTTTGTCTTTCATTAAGATGGAAGAAAGTGGACAGAGTTGTTGTTGCCAAGAAA 372

QY 347 GACGAGCTCGGAGCGCGCTCAGGAAGTACGCGCGCTGCGCAGTACGACGCTCCTGCC 406

Db 373 GAGGAGTTGCGAGACCATAGTGAAGCATGCTGCTCTCTACTGTCACTGCTTGAATC 432

QY 407 TC 408

Db 433 TC 434

## RESULT 8

US-08-449-315-103

; Sequence 103, Application US/08449315

; Patent No. 5650505

## GENERAL INFORMATION:

; APPLICANT: Ryals, John A.

; APPLICANT: Alexander, Danny C.

; APPLICANT: Beck, James J.

; APPLICANT: Duesing, John H.

; APPLICANT: Friedrich, Leslie B.

; APPLICANT: Goodman, Robert M.



;; TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
;; NUMBER OF SEQUENCES: 106  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: CIBA-GEIGY Corporation  
;; STREET: 7 Skyline Drive  
;; CITY: Hawthorne  
;; STATE: New York  
;; COUNTRY: USA  
;; ZIP: 10532  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/444,803  
;; FILING DATE: 19-MAY-1995  
;; CLASSIFICATION: 536  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/181,271  
;; FILING DATE: 13-JAN-94  
;; APPLICATION NUMBER: US 08/093,301  
;; FILING DATE: 16-JUL-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/937,197  
;; FILING DATE: 6-NOV-1992  
;; PRIOR APPLICATION DATA: US 07/678,378  
;; FILING DATE: 1-APR-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/305,566  
;; FILING DATE: 6-FEB-1989  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/165,667  
;; FILING DATE: 8-MAR-1988  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/042,847  
;; FILING DATE: 6-APR-1993  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/632,441  
;; FILING DATE: 21-DEC-1990  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/425,504  
;; FILING DATE: 20-OCT-1989  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/848,506  
;; FILING DATE: 6-MAR-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/768,122  
;; FILING DATE: 27-SEP-1991  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/580,431  
;; FILING DATE: 7-SEP-1990  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/368,672  
;; FILING DATE: 20-JUN-1989  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/329,018  
;; FILING DATE: 24-MAR-1989  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/045,957  
;; FILING DATE: 12-APR-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Elmer, James Scott  
;; REGISTRATION NUMBER: 36,129  
;; REFERENCE/DOCKET NUMBER: S-19825/P1/COC 1727  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (919)541-8614  
;; TELEFAX: (919)541-8689  
;; INFORMATION FOR SEQ ID NO: 103:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 653 base pairs  
;; TYPE: nucleic acid

;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
US-08-444-803-103  
Query Match 12.5%; Score 87.6; DB 1; Length 653;  
Best Local Similarity 54.4%; Pred. No. 2.7e-09;  
Matches 197; Conservative 0; Mismatches 164; Indels 1; Gaps 1;  
QY 48 CCGAGGAGGGTGGCGTGGATCGGTGCCACACCAAGGACGAGTTCGACCCCGCATGGCCA 107  
DB 73 CCGAGGAGGGACAAGTGTTCGGCTGCCACAAGGTTGAGGAATGGAACGAGTACTTCAAGA 132  
QY 108 AGGCCAAGGAGCAGGGCAAGCTGTGGTGCATCGCATTCATGGCCCCCTGGTGCAGTGGGT 167  
DB 133 AAGGCGTTGAGACTAAGAAACTGGTGGTGGTATTTTACTGCTTCATGGTGGCGSCCTT 192  
QY 168 GCCAGATGATGCCCGCGGTGTACGGGACTGGCCAGCAGTACCTTCCGCGGTCTTCC 227  
DB 193 GCCGTTTATTGCCCCCAATTCTTGTGACATTCCTTGAAGATGCCCATGTTATATTC 252  
QY 228 TCGAGTTCGACGTTCGACCAACTGTCTGGAAAGTGC - GAAGATCTACGGCGTCCATGTGATG 286  
DB 253 TCAGGTTTGATGTGATGAACCTGAAGACTGTTTCAGCGGGAATGGAGTGTGGAGGCAATG 312  
QY 287 CCGACCTTCTGCTTCATCAGGACCGCGAGACGCTCGAGAGCTTTGCTACCGTCCGACGAG 346  
DB 313 CCAACTTTTGTCTTCATTAAGATGGAAGAAAGAGTGGACAGAGTGTGTCGCCAAGAA 372  
QY 347 GACGAGCTCCGGAGCGCCCTCAGGAAGTACGGCGCGCTGGCACTACGACGGCTCCTGCC 406  
DB 373 GAGGAGTTCGACGACGACCATAGTGAAGCATGCTGCTCCTGCTACTGTCACTGCTTGAATC 432  
QY 407 TC 408  
DB 433 TC 434

RESULT 10  
US-08-449-043-103  
; Sequence 103, Application US/08449043  
; Patent No. 5689044  
; GENERAL INFORMATION:  
; APPLICANT: Ryals, John A.  
; APPLICANT: Alexander, Danny C.  
; APPLICANT: Beck, James J.  
; APPLICANT: Duesing, John H.  
; APPLICANT: Friedrich, Leslie B.  
; APPLICANT: Goodman, Robert M.  
; APPLICANT: Harms, Christian  
; APPLICANT: Meins, Jr., Frederick  
; APPLICANT: Montoya, Alice  
; APPLICANT: Moyer, Mary B.  
; APPLICANT: Neuhaus, Jean-Marc  
; APPLICANT: Payne, George B.  
; APPLICANT: Sperison, Christoph  
; APPLICANT: Stinson, Jeffrey R.  
; APPLICANT: Uknes, Scott J.  
; APPLICANT: Ward, Eric R.  
; APPLICANT: Williams, Shericka C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/449,043  
FILING DATE: 24-MAY-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/305,566  
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PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 541-8614  
TELEFAX: (919) 541-8689  
INFORMATION FOR SEQ ID NO: 103:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 653 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-449-043-103

Query Match 12.5%; Score 87.6; DB 1; Length 653;  
Best local Similarity 54.4%; Pred. No. 2.7e-09;  
Matches 197; Conservative 0; Mismatches 164; Indels 1; Gaps 1;  
Qy 48 CCGAGGAGGCGCGCTGATCGCTGCACACCAAGCAGGTTCCAGCGCCCGCATGGCCA 107  
Db 73 CCGAGGAGGACACAGTCTTCGCTGCCACACAGGTTGAGGATGCAAGAGTACTTCAAGA 132

Qy 108 AGGCAAGAGGACGAGCGCAAGCTGGTGTCTATGCACTTTCATGCGCCCTGCTGAGTGGGT 167  
Db 133 AAGCGTTGAGACTAAGAACTGCTGGTGGTGGATTTTACTGCTTCAATGCTGGGSCCTT 192  
Qy 168 GCCAGATGATGGCCCGGCTGTACGCGGACTGCGCAGCAAGTACCCCTTCCGCGGTCTTCC 227  
Db 193 GCCGTTTATTTGCCCAATTTCTGCTGNCATTGCTAAGAGATGCCCATGTTATATTC 252  
Qy 228 TCGAGGTGAGCTGCGACGAACCTGCTGGAGTCGG- GAAGATCTACGGCGTCCATGTGATG 286  
Db 253 TCAAGGTTGATGTTGATGAAGTGAAGACTCTTTTTCAGCGGGAATGGAGTGTGGAGCAATG 312  
Qy 287 CCGACCTTCTGCTTTCATCAGACGCGGAGACGCTCGAGAGCTTTTGTACCGTCGACGAG 346  
Db 313 CCAACTTTTCTTTCATTAAGATGGAAGAGAAAGTGGACAGAGTTGTTGGTGCCAGAAA 372  
Qy 347 GACGAGCTCGGAGCGGCTGAGAGTACGCGCGCTGCGACTAGCAGCGGTCTCTGCC 406  
Db 373 GAGGAGTTGCAGCAGACCATAGTGAAGCATGCTCTCTCTACTGTCTACTGCTTGAATC 432  
Qy 407 TC 408  
Db 433 TC 434  
RESULT 11  
US-08-456-265A-103  
Sequence 103, Application US/08456265A  
Patent No. 5767369  
GENERAL INFORMATION:  
APPLICANT: Alexander, Danny C.  
APPLICANT: Ryals, John A.  
APPLICANT: Goodman, Robert M.  
APPLICANT: Stinson, Jeffrey R.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 520 White Plains Road, P.O. Box 2005  
CITY: Tarrytown  
STATE: New York  
COUNTRY: USA  
ZIP: 10591  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/456,265A  
FILING DATE: 31-MAY-95  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/181,271  
FILING DATE: 13-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:



APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIOR APPLICATION DATA: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727/DIV10  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8587  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 103:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 653 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-456-265A-103

Query Match 12.5%; Score 87.6; DB 1; Length 653;  
Best Local Similarity 54.4%; Pred. No. 2.7e-09;  
Matches 197; Conservative 0; Mismatches 164; Indels 1; Gaps 1;

Qy 48 CCGAGGAGGTCGCGTATCGCGTCCACACCAAGGACGAGTTGCGAGCCCGCATGCCCA 107  
Db 73 CCGAGGAGGACAAAGTGTTCGCTGCCACAAAGTTGAGGAATGGAACGAGTACTTCAAGA 132  
Qy 108 AGCGCAGGACGAGGCGAAGTGTGTCTCATGTCGCGCCCTCGTGCAGTGGGT 167  
Db 133 AAGCGTTGAGACTTAAGAACTGTGTGTGTGTCTGTCTCTCATGTGCGGSCCTT 192  
Qy 168 GCCAGATGATGCGCCCGGTGTACCGGAGTGCAGCAAGTACCCCTTCGCGGTCTTCC 227  
Db 193 GCGCTTTATTTGCCCAATCTTCTGACATTTCTAAGAAAGATGCCCAATGTTATATTC 252  
Qy 228 TCGAGGTGCGCTCGAGCACTGTGAGTCCG-AGAGTCTACGCGTCCATGTGATG 286  
Db 253 TCAAGGTTGATGTTGATGAATGAAGTGTTCAGCGGATGAGTGTGGAGCAATG 312  
Qy 287 CCGACCTTCTGCTTCATCAGGAACGGCGAGACGCTCGAGAGCTTTGTTCGTCGAGAG 346  
Db 313 CCACTTTTGTCTTCAITAAAGATGGAAGAGTGGACAGTGTGTTGTGCGCAAGAA 372  
Qy 347 GACGAGTCCGGAGCGCGTCAAGAGTACCGCCGCTGGCACTACGAGGCTCTGCC 406  
Db 373 GAGGAGTTGCAGCAGACCATAGTGAAGCATGCTGCTCTACTGCTACTGCTGTAATC 432  
Qy 407 TC 408  
Db 433 TC 434

RESULT 12  
US-08-455-416-103  
Sequence 103: Application US/08455416  
Patent No. 5777200  
GENERAL INFORMATION:  
APPLICANT: Ryals, John A.  
APPLICANT: Alexander, Danny C.  
APPLICANT: Beck, James J.  
APPLICANT: Duesing, John H.  
APPLICANT: Friedrich, Leslie B.  
APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uxnes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,416  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
FILING DATE: 6-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/678,378  
FILING DATE: 1-APR-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/305,566  
FILING DATE: 6-FEB-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8614  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 103:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 653 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-455-416-103

Query Match 12.5% Score 87.6; DB 1; Length 653;  
Best Local Similarity 54.4%; Pred No. 2.7e-09;  
Matches 197; Conservative 0; Mismatches 164; Indels 1; Gaps 1;  
QY 48 CCGAGGAGGTCGCTGATCCGTCGACACCAAGGACGAGTTCGACGCCCGCATGGCCA 107  
Db |||||  
73 CCGAGGAGGACAAAGTCTTCGGCTGCCACAAAGTTGAGGAATGGAACGAGTACTTCAAGA 132  
QY 108 AGCCAGGAGGACGAGGCGGACGCTGCTGTCATCGACTTCATGCCCCCTGCTGCTGCTGCT 167  
Db |||||  
133 AGCGCTTGAGACTAGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 192  
QY 168 GCGAGATGATGCGCCCGCTGATCGCGGCTGCGCCGACGAGTACCTTCGCGGCTCTCC 227  
Db |||||  
193 GCGCTTTTATGCGCCCAATTCCTGCTGACATTCCTAAGGATGCGCCCATGTTATATTC 252  
QY 228 TCGAGTTCGAGTCGACGAGTCTGGAAGTCG-CAAGATCTACGGGTCCTCATGTGATG 286  
Db |||||  
253 TCAAGTTGATGTTGATGAACTGTAAGTCTTTTACGGGAAATGAGTGTGGAGCAATG 312  
QY 287 CCGACCTTCTGCTTCATCAGGAACGCGGACGCTCGAGAGCTTTCTACCGTCCAGCAG 346  
Db |||||  
313 CCAACTTTCTCTTCATTAAGATGGAAGAAAGTGGACAGAGTGTGTTGGTCCCAAGAA 372  
QY 347 GACGAGTCCGGGACGCGCTCAGAGTACGCGCGCTGCGCACTACGAGCGCTCTGCC 406  
Db |||||  
373 GAGAGTTGACGAGACCAATAGTGAAGCATGCTGCTCTCTGCTACTGTCTACTGTAATC 432  
QY 407 TC 408  
Db ||  
433 TC 434

## RESULT 13

US-08-455-244-103  
Sequence 103, Application US/08455244  
Patent No. 5789214  
GENERAL INFORMATION:  
APPLICANT: Ryals, John A.  
APPLICANT: Alexander, Danny C.  
APPLICANT: Beck, James J.  
APPLICANT: Duesing, John H.  
APPLICANT: Friedrich, Leslie B.

APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.  
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible-  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,244  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
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APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT 1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
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PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:

TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC  
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF  
NUMBER OF SEQUENCES: 106  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/454,876  
FILING DATE: 31-MAY-1995

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/181,271  
FILING DATE: 13-JAN-94  
APPLICATION NUMBER: US 08/093,301  
FILING DATE: 16-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/937,197  
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APPLICATION NUMBER: US 07/165,667  
FILING DATE: 8-MAR-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/042,847  
FILING DATE: 6-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/632,441  
FILING DATE: 21-DEC-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/425,504  
FILING DATE: 20-OCT-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/848,506  
FILING DATE: 6-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/768,122  
FILING DATE: 27-SEP-1991  
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APPLICATION NUMBER: US 07/580,431  
FILING DATE: 7-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/368,672  
FILING DATE: 20-JUN-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/329,018  
FILING DATE: 24-MAR-1989  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993

ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: S-19825/PL/CGC 1727  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8614  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 103:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 653 base pairs

APPLICATION NUMBER: US 08/045,957  
FILING DATE: 12-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Elmer, James Scott  
REGISTRATION NUMBER: 36,129  
REFERENCE/DOCKET NUMBER: S-19825/PL/CGC 1727  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8614  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 103:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 653 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-455-244-103

Query Match 12.5%; Score 87.6; DB 1; Length 653;  
Best Local Similarity 54.4%; Pred. No. 2.7e-09;  
Matches 197; Conservative 0; Mismatches 164; Indels 1; Gaps 1;

QY	48	CCGAGGAGGCGCGGTGATCGCGTGCACACCAAGGACGAGTTTCGACGCCCGCATGGCCA	107
DB	73	CCGAGGAGGACAAAGTGTTCGGCTGCCACAGGTTGAGGAATGGAACGAGTACTTCAAGA	132
QY	108	AGGCCAAGGAGCGGCAAGCTGGTGCATCGACTTCATGCGCCCTCGTGCAGTGGGT	167
DB	133	AAGCGCTTGAGACTAAGAAACTGGTGGTGCATTTTACTGCTTCATGGTGGGSCCTT	192
QY	168	GCCAGATGATGGCCCGGTGACGCGACTGCGCCAGCAAGTACCTTCGCGCGTCTTCC	227
DB	193	GCGGTTTATGCCCCAATCTTCTGTCATCTAAGAGATGCCCATGTTATATTC	252
QY	228	TCGAGTTCGAGTCGACGAACTCTGGAAGTGC-GAAGATCTACGCGGTCGATGATG	286
DB	253	TCAAGGTTGATGTTGATGAATGAATGAATGAATGAATGAATGAATGAATGAATG	312
QY	287	CCGACCTTCGCTTCATCAGGACGCGGAGAGCTTCGAGAGCTTGTCTACCGTCGACGAG	346
DB	313	CCAACTTTCTCTTCATTAAGATGGAAGAGAGTGGAGATTTGTTGGTCCAGAA	372
QY	347	GACGAGTCCGGAAGCGCGTCAGGAAGTACGCGCGCTGGCACTACGAGCGCTCTCC	406
DB	373	GAGGAGTTGCAGCAGACCAATAGTGAAGCATGCTGCTCTCTACTGTCACTGCTTGAATC	432
QY	407	TC 408	
DB	433	TC 434	

RESULT 14  
US-08-454-876-103  
Sequence 103, Application US/08454876  
Patent No. 5804693  
GENERAL INFORMATION:  
APPLICANT: Ryals, John A.  
APPLICANT: Alexander, Danny C.  
APPLICANT: Beck, James J.  
APPLICANT: Duesing, John W.  
APPLICANT: Friedrich, Leslie B.  
APPLICANT: Goodman, Robert M.  
APPLICANT: Harms, Christian  
APPLICANT: Meins, Jr., Frederick  
APPLICANT: Montoya, Alice  
APPLICANT: Moyer, Mary B.  
APPLICANT: Neuhaus, Jean-Marc  
APPLICANT: Payne, George B.  
APPLICANT: Sperison, Christoph  
APPLICANT: Stinson, Jeffrey R.  
APPLICANT: Uknes, Scott J.  
APPLICANT: Ward, Eric R.  
APPLICANT: Williams, Shericca C.



Db	73	CCGAGGAGGACAAAGTGTTCGGCTGCCACAAGTTGAGGAATGGAACGAGTACTTCAAGA	132
Qy	108	AGCCCAAGAGAGAGGCAAGCTGGTGGTCATCGACTTCATGGCCCCCTGGTGCAGTGGGT	167
Db	133	AAGGCGTTGAGACTAAGAAACTGGTGGTGGTGAATTTACTGCTTCATGGTGGGSCCTT	192
Qy	168	GCCAGATGATGGCCCCGGTGTACGCGGACTGCGCCACAGTACCCCTTCGGGGTCTTCC	227
Db	193	GCCGTTTTATTGCCCCCAATTCCTTGCTGACATTCCTAAGAAGATGCCCATGTTATATTCC	252
Qy	228	TCGAGTGGACGTCGACGAACTGGTGGAGTCCG-GAAGATCTACGGCGTCCATGTGATG	286
Db	253	TCAAGGTTGATGTTGATGAATCTGAAGACTGTTTCAGCGGAATGGAGTGTGGAGGCAATG	312
Qy	287	CCGACCTTCTGCTTCATCAGGACGGCGAGACGCTCGAGAGCTTTGCTACCGTCGACGAG	346
Db	313	CCACTTTTGCTCTTCATTAAGATGGAAGAAGTGGACAGATTGTTGGTGCCAAAGAA	372
Qy	347	GACGAGCTCCGGGAAGCGGTCAGGAAGTACGCGCGCGCTGGCACTACGAGCGCTCCTGCC	406
Db	373	GAGGAGTTGCAGCAGACCATAGTGAAGCATGCTGCTCCTGCTACTGTCACTGCTTGAATC	432
Qy	407	TC	408
Db	433	TC	434

Search completed: May 5, 2004, 23:29:36  
Job time : 60.7917 secs

1	613	87.6	731	13	US-10-425-114-16798	Sequence 16738, A
2	613	87.6	742	13	US-10-425-114-16904	Sequence 16904, A
3	613	87.6	752	13	US-10-425-114-17028	Sequence 17028, A
4	492.4	70.3	780	13	US-10-425-114-7100	Sequence 7100, App
5	379.4	54.2	647	13	US-10-425-114-18407	Sequence 18407, A
6	208.8	29.8	737	13	US-10-425-114-35090	Sequence 35090, A
7	207.2	29.6	548	13	US-10-425-114-23500	Sequence 23500, A
8	207.2	29.6	588	13	US-10-425-114-23471	Sequence 23471, A
9	207.2	29.6	591	13	US-10-425-114-23458	Sequence 23458, A
10	205.6	29.4	565	13	US-10-425-114-35828	Sequence 35828, A
11	205.6	29.4	577	13	US-10-425-114-6528	Sequence 6528, App
12	205.6	29.4	583	13	US-10-425-114-284	Sequence 284, App
13	205.6	29.4	594	13	US-10-425-114-17618	Sequence 17618, A
14	205.6	29.4	692	13	US-10-425-114-23337	Sequence 23337, A



DB	76	CGTGATCGCGTCCACACACAGAGCAGAGTTCGAGCGCCGATGCGCAAGGCCAAGGAGCA	135
QY	121	GGGCAAGCTGGTGGTTCATCGACTTCATGCGCCCGCTGGTGCGAGTGGGTGCCAGATGATGGC	180
DB	136	GGGCAAGCTGGTGGTTCATCGACTTCATGCGCCCGCTGGTGCGAGTGGGTGCCAGATGATGGC	195
QY	181	CCCGGTGTACGCGGACTGCGCGCAGCAAGTACCCTTCCCGGTCCTCCGAGGTCGACGT	240
DB	196	CCCGGTGTACGCGGACTGCGCGCAGCAAGTACCCTTCCCGGTCCTCCGAGGTCGACGT	255
QY	241	CGACGCAACTGCTGGAAAGTCCGCAAGATCTACGGCGTCATGTGATGCGGACCTTCTGCTT	300
DB	256	CGACGCAACTGCTGGAAAGTCCGCAAGATCTACGGCGTCATGTGATGCGGACCTTCTGCTT	315
QY	301	CATCAGGAACGGCGAGACCGCTCGAGAGCTTTGCTACCGTCCAGCAGACGAGCTCCCGGA	360
DB	316	CATCAGGAACGGCGAGACCGCTCGAGAGCTTTGCTACCGTCCAGCAGACGAGCTCCCGGA	375
QY	361	CGCGCTCAGGAAGTACGCGCGCGCTGGGCACTACGACGGCTCCTGCCTCGCGTCGCGCTA	420
DB	376	CGCGCTCAGGAAGTACGCGCGCGCTGGGCACTACGACGGCTCCTGCCTCGCGTCGCGCTA	435
QY	421	ATTTCAGGAGATGTGATGCTAGCAATAATAGCGCGCGCACCCAGTCGTCAATAATAAATA	480
DB	436	ATTTCAGGAGATGTGATGCTAGCAATAATAGCGCGCGCACCCAGTCGTCAATAATAAATA	487
QY	481	AATAAATAAATAAATAAATAAATAAATAAAGGCCAACGTCACGACGCAAAATTAGTG	540
DB	488	AATAAATAAATAAATAAATAAATAAATAAAGGCCAACGTCACGACGCAAAATTAGTG	547
QY	541	GCSCGCGCGGTAGTAGTACGACAGTATGCGCGGCCACTGTGTGCGATCTCAGTTTGGTC	600
DB	548	GCSCGCGCGGTAGTAGTACGACAGTATGCGCGGCCACTGTGTGCGATCTCAGTTTGGTC	607
QY	601	GTTTAAAGTAGATTGATGTGTACTATGTTCCAGTCGA	639
DB	608	GTTTAAAGTAGATTGATGTGTACTATGTTCCAGTCGA	646

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RESULT 4
US-10-425-114-7100
; Sequence 7100, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53113) B
; CURRENT APPLICATION NUMBER: US/10/425.114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 7100
; LENGTH: 780
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700617241_FLI
US-10-425-114-7100

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	Query Match	70.3%	Score 492.4	DB 13	Length 780
	Best Local Similarity	92.4%	Pred. No. 1.9e-99		
	Matches 606	Conservative 16	Mismatches 0	Indels 34	Gaps 7
Qy	1	GGATCCCAACCCGAGG-----AAGGAGAGAGAGGGTTCGGAAATATATGCGGCGCCGAGGAG	55		
Db	57	GGATCCCAACCCGAGGAAATTAAGGAGAGAGAGGGTTCGGAAATATGCGGCGCCGAGGAG	116		
Qy	56	GGTCCCGTGTCCGTGCGACCAACGAGAGAGTTCGACGCCGCCGATGCGCAAGGCCAAG	115		

[illegible]

```

RESULT 5
US-10-425-114-18407
; Sequence 18407, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(533131B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 18407
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3079-042-Cl_FLI
US-10-425-114-18407

```

	Query Match	54.2%	Score 379.4;	DB 13;	Length 647;
	Best Local Similarity	95.5%;	Pred.No. 2.le-74;		
	Matches 404;	Conservative 0;	Mismatches 11;	Indels 8;	Gaps 1
Qy	217	C G C G T C T T C T C A G C T T C G A C T C G N C G A C T C G T G G A G T C G C G A A G T C T A C G G C G T	276		
Dd	148	C C G C G G C A G C C G C G C A T C G A C G T G C G A A C T G C T G G A A G T C G C G A A G T C T A C G G C G T	207		



277	QY	CCATGTGATGCGGACCTTCTGCTTCATCAGAA	CGCGAGACGCTCGAGAGCTTTGCTTAC	336
208	Db	CCATGTGATGCGGACCTTCTGCTTCATCAGAA	CGCGAGACGCTCGAGAGCTTTGCTTAC	267
337	QY	CGTCGACGAGCAGAGCTCCGGGCGCGCTCAG	AGTAGCGCGCTGGCACTACGAC	396
268	Db	CGTCGACGAGCAGAGCTCCGGGCGCGCTCAG	AGTAGCGCGCTGGCACTACGAC	327
397	QY	GGCTCCTCGCTCGGCGTCCGCTTAATTCAG	GAGATGTGTAGCAATAAGCGCGGC	456
328	Db	GGCTCCTCGCTCGGCGTCCGCTTAATTCAG	GAGATGTGTAGCAATAAGCGCGGC	387
457	QY	GCACGAGTGGTCATATAATAATAATAATAA	TAAATAATAATAATAATAAAGG	516
388	Db	GCACGAGTGGTC-----AATAATAATAA	TAAATAATAATAATAATAAAGG	439
517	QY	CCAAAGTACGACCAAAATTAGTCGCGCGCG	CTGTAGCTAGCAGAGTAGCGCGCGC	576
440	Db	CCAAAGTACGACCAAAATTAGTCGCGCGCG	CTGTAGCTAGCAGAGTAGCGCGCGC	499
577	QY	ACTGTGTCGATCTGCAGTTTGGTGTTTAA	AGTAGATTGTAGTGTACTATGTTCA	636
500	Db	ACTGTGTCGATCTGCAGTTTGGTGTTTAA	AGTAGATTGTAGTGTACTATGTTCA	559
637	QY	CGA	639	
560	Db	CGA	562	

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RESULT 6
US-10-425-114-35090
  ; Sequence 35090, Application US/10425114
  ; Publication No. US20040034888A1
  ; GENERAL INFORMATION:
  ; APPLICANT: Liu, Jingdong
  ; APPLICANT: Zhou, Yihua
  ; APPLICANT: Kowalic, David K.
  ; APPLICANT: Screen, Steven E
  ; APPLICANT: Tabaska, Jack E
  ; APPLICANT: Cao, Yongwei
  ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
  ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
  ; FILE REFERENCE: 38-21(53313)B
  ; CURRENT APPLICATION NUMBER: US/10/425,114
  ; CURRENT FILING DATE: 2003-04-28
  ; NUMBER OF SEQ ID NOS: 73128
  ; SEQ ID NO 35090
  ; LENGTH: 737
  ; TYPE: DNA
  ; ORGANISM: Zea mays subsp. mexicana
  ; FEATURE:
  ; OTHER INFORMATION: Clone ID: UC-ZMFLTBOSINTE079E09_FLI
  ; US-10-425-114-35090

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	Query Match.	29.8%;	Score 208.8;	DB 13;	Length 737;
	Best Local Similarity	72.6%;	Pred. No. 1.5e-36;		
	Matches 270;	Conservative 0;	Mismatches 102;	Indels 0;	Gaps 0;
QY	36	GAATAATGGCGGCGGAGAGGGTCCCTGATCGGCTGCCACACCAAGGACGAGTTCGACG	95		
Db	86	GATCAATGGGCTCCGACAGGGAGTCGTGATCGGCTGCCACCAAGCTGAGTTCGACG	145		
QY	96	CCGCGATCGGCCAAGGCCAAGAGCAGGGCAAGCTGGTGGTCATCGACTTCAATGCCGCCCT	155		
Db	146	CCCAATGACCAAGGCCAGGAAGCCCGCAAGCTGGTGGTCATCGACTTCAATCCCGGCT	205		
QY	156	GGTGCAGTGGGTGCGCAGATGATGCCCGCGGTGTACGGCGAGTGGCGCAGCAAGTACCCCTT	215		
Db	206	GGTGGGTGCCATGCGCGGGCCATCGCCCACTGTTTCTGTGCGAACACGCCAGGAAGTTCATCT	265		
QY	216	CCGGGGTCTTCTCTCGAGTCCAGCTCGACGAACCTGCTGGAAGTGGCGAAGATCTACCGCG	275		
Db	266	AGGTGGTCTTCTCTGAAAGTGGAGCTGGACGAAGTGAAGGAAGTCAACCGCGGCTTACGAGG	325		

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276  TCATGTGATGCCGACCTTCTGCTTCATCAGGAACGGCGAGACGCTCGAGAGCTTTGCTA 335
Db   TCAGGCGGATGCCGACCTTCCACTTCGTTCAAGAACGGCAAGACGGTCGCGACCATCGTGG 385
Qy   CCCTGTGACGAGGACGAGCTCCGGGAGCCCGTCAGAAAGTACGCCGCGCGCTGGCACTACGA 395
Db   GTGCCAGAGGACGAGCTCTGSCCTTGATCGAAGACATGCCGCGCTTGGCGCTCGCT 445
Qy   CGGCTCCTCGCT 407
Db   CTGCGTCTGCT 457

RESULT 7
US-10-425-114-23500
; Sequence 23500, Application US/10425114
; Publication No. US20040034889A1
; GENERAL INFORMATION:
; APPLICANT: Lili, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 23500
; LENGTH: 548
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB9596-057-G4_FLI
US-10-425-114-23500

```

Query Match	29.6%;	Score	207.2;	DB	13;	Length	548;
Best Local Similarity	72.3%;	Pred. No.	3e-36;				
Matches	269;	Conservative	0;	Mismatches	103;	Indels	0;
Gaps	0;						
Qy	36	GAATAATGGCGGCGGAGGAGGGTGCCTGATCGGTGCACACCAAGGACGAGTTGCACG	95				
Db	55	GATCAATGGGTCCGAGCAGGGAGTCTGTATTCGGTCCACACGCAAGGCTGAGTTGCACG	114				
Qy	96	CCGCGATGGCCAAAGGCCAAGGAGCAGGGCAAGCTGTGGTTCATCGACTTCATGGCCCCCT	155				
Db	115	CCACATGACCAAGGCCCAGGAAGCCGGAAGCTGTGGTTCATCGACTTCACATGCCGCCT	174				
Qy	156	GGTGCAGTGGTCCAGATGATCGGCCCGGTGTACGGGACTCGCGCAGCAAGTACCCCTT	215				
Db	175	GGTSCGGTCCATGCCCGGCCATCGCCCACTGTTCTGCGAACACGCCCAAGATTCATCTC	234				
Qy	216	CCGCGGTCTTCCTCGAGGTGCGACTCGACAACTGCTGGAAGTTCGGGAAAGATCTACGGCG	275				
Db	235	AGGTGCTCTTCTGAAGGTGGACGTGGACGAAGTGAAGGAAGTCAACGGCGCCCTACGAGG	294				
Qy	276	TCAATGTATGCCGACCTTCTGCTTCATCGGAAACGGCGAGAGCTTCGAGAGTTTGTCTA	335				
Db	295	TCGAGGCGATGCCGACCTTCCTCACTTCGTCAGAAACGGCAAGACGGTTCGACCATCGTGG	354				
Qy	336	CCGTTCACAGGACGAGCTCCGGGAGCCGCTCAGGAAGTACGCGCGCGGTGGCACTACGA	395				
Db	355	GTGCCAAGAGGACGAGCTCTGGCCCTGATCGAAGGATGCGCGGCCCTCGCGCTCGCT	414				
Qy	396	CGGCTCTGCT	407				
Db	415	CTGGCTGCT	426				

RESULT 8

```

? APPLICANT: Tabaska, Steven E
? APPLICANT: Tabaska, Jack E
? APPLICANT: Cao, Yongwei
? TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
? TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
? FILE REFERENCE: 38-21(53313)B
? CURRENT APPLICATION NUMBER: US/10/425,114
? CURRENT FILING DATE: 2003-04-28
? QUERY MATCH          29.4%; Score 205.6; DB 13; Length 565;
? Best local Similarity 72.0%; Pred. No. 6.8e-36;
? Matches 268; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
? QY      36   GAATAATGGCGCAGGAGGTGGCTGATCGTGCACACCACCAAGCACGATTTCGACG 95

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Db 30 GATCATGCGCTCCGAGCAGGAGTCTGTATCGCTGCCACAGCAAGGCTGAGTTTCGAGC 89  
Qy 96 CCCGCTATGCGCAAGGCCAGAGCAGGCTGCTGTGCTCATCGACTTCATGCGCCCT 155  
Db 90 CCACATGACCAAGGCCAGAGCAGGCTGCTGTGCTCATCGACTTCATGCGCCCT 149  
Qy 156 GGTGCAAGTGGTCCAGATGATGCGCCCGTGTACGCGAGTCTGCGCAGCAAGTACCCCTT 215  
Db 150 GGTGCGGTCCATGCGCGCCATCGCCCACTGTTCGTGCAACACGCCAAGAGTTCACTC 209  
Qy 216 CCGCGGTCTTCCTCGAGTCCGCTGCGAGTCTGCTGGAAGTCCGAGATCTACGCG 275  
Db 210 AGTGTCTCTCTGAGAGTGGAGTGGAGAGTGAAGAGTCAACCGCGCTACGAGG 269  
Qy 276 TCCATGTATGCGCACTTCTGCTTCATCAGGAACGCGAGAGCTGCTGAGAGCTTTGCTA 335  
Db 270 TCGAGGCGATCGCGCACTTCCACTTCGTCAAGAACGCGCAAGCGGTGCGACCATCGTGG 329  
Qy 336 CCGTCGACGAGGAGCTCCGCGAGCGCTCAGGAAGTCTGAGAGTACGCGCTGCCACTAGA 395  
Db 330 GTGCCAGGAGGAGGAGCTCTGCGCCCATCGAGATCGAGAGCATCGCGCGCTGCGCT 389  
Qy 396 CGCTCTCTGCT 407  
Db 390 CTGCTCTGCT 401

RESULT 11  
US-10-425-114-6528  
; Sequence 6528, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 6528  
; LENGTH: 577  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700570172\_FLI  
US-10-425-114-6528

Query Match 29.4%; Score 205.6; DB 13; Length 577;  
Best Local Similarity 72.0%; Pred. No. 6.9e-36;  
Matches 268; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

Qy 36 GAATATGCGCGCCGAGGAGGCTGCTGATCGCTGCCACCAAGCAAGGCTGAGTTTCGAGC 95  
Db 40 GATCATGCGCTCCGAGCAGGAGTCTGTATCGCTGCCACAGCAAGGCTGAGTTTCGAGC 99  
Qy 96 CCGCATGCGCCAGGCCAGAGCAGGCTGCTGTGCTCATCGACTTCATGCGCCCT 155  
Db 100 CCACATGACCAAGGCCAGAGCAGGCTGCTGTGCTCATCGACTTCATGCGCCCT 159  
Qy 156 GGTGCAAGTGGTCCAGATGATGCGCCCGTGTACGCGAGTCTGCGCAGCAAGTACCCCTT 215  
Db 160 GGTGCGGTCCATGCGCGCCATCGCCCACTGTTCGTGCAACACGCCAAGAGTTCACTC 219  
Qy 216 CCGCGGTCTTCCTCGAGTCCGCTGCGAGTCTGCTGGAAGTCCGAGATCTACGCG 275  
Db 220 AGTGTCTCTCTGAGAGTGGAGTGGAGAGTGAAGAGTCAACCGCGCTACGAGG 279  
Qy 276 TCCATGTATGCGCACTTCTGCTTCATCAGGAACGCGAGAGCTGCGCAGCAAGTACCCCTT 335

Db 280 TCGAGGCGATGCCGACCTTCCACTTCGTCAAGAACCGCAAGAGCGGTCCGACCATCGTG 339  
Qy 336 CCGTCGAGCAGGAGCGCTCCGCGAGCGCGTCAAGAGTACCGCGCGTGGCACTACGA 395  
Db 340 GTGCCAGGAGGAGGAGCTCTGCGCCCTGATCGAGAGCATCGCGCGCTGCGCTCGCA 399  
Qy 396 CGCTCTCTGCT 407  
Db 400 CTGCGTCTGCT 411

RESULT 12  
US-10-425-114-284  
; Sequence 284, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 284  
; LENGTH: 583  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 700052149\_FLI  
US-10-425-114-284

Query Match 29.4%; Score 205.6; DB 13; Length 583;  
Best Local Similarity 72.0%; Pred. No. 6.9e-36;  
Matches 268; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

Qy 36 GAATATGCGCGCCGAGGAGGCTGCTGATCGCTGCCACCAAGCAAGGCTGAGTTTCGAGC 95  
Db 42 GATCATGCGCTCCGAGCAGGAGTCTGTATCGCTGCCACAGCAAGGCTGAGTTTCGAGC 101  
Qy 96 CCGCATGCGCCAGGCCAGAGCAGGCTGCTGTGCTCATCGACTTCATGCGCCCT 155  
Db 102 CCACATGACCAAGGCCAGAGCAGGCTGCTGTGCTCATCGACTTCATGCGCCCT 161  
Qy 156 GGTGCAAGTGGTCCAGATGATGCGCCCGTGTACGCGAGTCTGCGCAGCAAGTACCCCTT 215  
Db 162 GGTGCGGTCTCATGCGCGCCATCGCCCACTGTTCGTGCAACACGCCAAGAGTTCACTC 221  
Qy 216 CCGCGGTCTTCCTCGAGTCCGCTGCGAGTCTGCTGGAAGTCCGAGATCTACGCG 275  
Db 222 AGTGTCTCTCTGAGAGTGGAGTGGAGAGTGAAGAGTCAACCGCGCTACGAGG 281  
Qy 276 TCCATGTATGCGCACTTCTGCTTCATCAGGAACGCGAGAGCTGCGAGAGTTTCGTA 335  
Db 282 TCGAGCGATGCGGACCTTCCACTTCGTCAAGAACGCGCAACCGCTCGGACCATCGTG 341  
Qy 336 CCGTCGAGCAGGAGCTCCGCGAGCGCGTCAAGAGTACGCGCGCTGCGCACTACGA 395  
Db 342 GTGCCAGGAGGAGGAGCTCTGCGCCCATCGAGATCGAGAGCATCGCGCGCTGCGCT 401  
Qy 396 CGCTCTCTGCT 407  
Db 402 CTGCGTCTGCT 413

RESULT 13  
US-10-425-114-17618  
; Sequence 17618, Application US/10425114

Publication No. US20040034888A1  
GENERAL INFORMATION:  
APPLICANT: Liu, Jingdong  
APPLICANT: Zhou, Yihua  
APPLICANT: Kovalic, David K.  
APPLICANT: Screen, Steven E  
APPLICANT: Tabaska, Jack E  
APPLICANT: Cao, Yongwei  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53313)B  
CURRENT APPLICATION NUMBER: US/10/425,114  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 73128  
SEQ ID NO 17618  
LENGTH: 594  
TYPE: DNA  
ORGANISM: Zea mays  
FEATURE:  
OTHER INFORMATION: Clone ID: LIB3070-001-09\_FLI  
US-10-425-114-17618

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Best Local Similarity 72.0%; Pred. No. 6.9e-36;  
Matches 268; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

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Db 113 CCCACATGACCAAGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 172  
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Db 233 AGTGTGTCCTTCTTCGAGGTCGAGCTGCGCGTGCATCGCGTGCACACCAAGAGTACCCCTT 292  
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QY 336 CCGTCGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 395  
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RESULT 14  
US-10-425-114-23337  
Sequence 23337, Application US/10425114  
Publication No. US20040034888A1  
GENERAL INFORMATION:  
APPLICANT: Liu, Jingdong  
APPLICANT: Zhou, Yihua  
APPLICANT: Kovalic, David K.  
APPLICANT: Screen, Steven E  
APPLICANT: Tabaska, Jack E  
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53313)B  
CURRENT APPLICATION NUMBER: US/10/425,114  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 73128  
SEQ ID NO 23337

LENGTH: 692  
TYPE: DNA  
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FEATURE:  
OTHER INFORMATION: Clone ID: LIB3595-039-B9\_FLI  
US-10-425-114-23337

Query Match 29.4%; Score 205.6; DB 13; Length 692;  
Best Local Similarity 72.0%; Pred. No. 7.4e-36;  
Matches 268; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY 36 GAATAATGCGCGCGAGGAGGTCGCGTGCATCGCGTGCACACCAAGAGGAGTTGCGAG 95  
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Db 71 CCCACATGACCAAGGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 130  
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Db 311 GTGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 370  
QY 396 CCGCTCTGCGCT 407  
Db 371 CTGCGTCTGCGCT 382

RESULT 15  
US-10-260-238-5754  
Sequence 5754, Application US/10260238  
Publication No. US20040016025A1  
GENERAL INFORMATION:  
APPLICANT: Budworth, Paul R.  
APPLICANT: Moughamer, Todd G.  
APPLICANT: Briggs, Steven P.  
APPLICANT: Cooper, Bret  
APPLICANT: Glazebrook, Jane  
APPLICANT: Goff, Stephen A.  
APPLICANT: Katagiri, Fumiyaki  
APPLICANT: Kreps, Joel  
APPLICANT: Provart, Nicholas  
APPLICANT: Rickes, Darrell  
APPLICANT: Zhu, Tong  
TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION  
FILE REFERENCE: 60111-NP  
CURRENT APPLICATION NUMBER: US/10/260,238  
CURRENT FILING DATE: 2002-09-26  
PRIOR FILING DATE: 2002-09-26  
PRIOR APPLICATION NUMBER: US 60/325,448  
PRIOR FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: US 60/325,277  
PRIOR FILING DATE: 2001-09-26  
PRIOR APPLICATION NUMBER: US 60/370,620  
PRIOR FILING DATE: 2002-04-04  
NUMBER OF SEQ ID NOS: 6077  
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TYPE: DNA  
ORGANISM: Zea mays  
US-10-260-238-5754

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Job time : 325.214 secs

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Job time : 325.214 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 5, 2004, 13:19:01 ; Search time 5435.21 Seconds  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

Database :

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Result 1  
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DEFINITION  
Oryza sativa (japonica cultivar-group) cDNA clone.001-024-C03, full  
insert sequence.  
AK104317  
ACCESSION  
VERSION  
FLI\_CDNA; oligo capping.  
KEYWORDS  
SOURCE  
Oryza sativa (japonica cultivar-group)  
ORGANISM  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriaristaceae; Oryzae; Oryza.

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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3	755.4	56.5	1383	8	AK106368	AK106368 Oryza sat
4	730.2	54.7	1045	8	TAB421947	AT421947 Triticum
5	709.6	53.1	118300	8	AP004165	AP004165 Oryza sat
6	708	53.0	1580	6	AX366999	AX366999 Sequence
7	684.4	51.2	1130	6	AX654214	AX654214 Sequence
8	683.4	51.2	131980	2	AP005477	AP005477 Oryza sat
9	623.4	46.7	963	6	AX653785	AX653785 Sequence
10	562.8	42.1	1021	6	AX366997	AX366997 Sequence
11	457	34.2	1152	6	AX507791	AX507791 Sequence
12	457	34.2	1152	6	AX651358	AX651358 Sequence
13	432.8	32.4	1433	8	BT004322	BT004322 Arabidops
14	421	31.5	1148	8	ATTHIRDA	Z23108 A.thaliana
15	410	30.7	76170	8	AC002329	AC002329 Arabidops
16	404	30.2	1128	8	AY099756	AY099756 Arabidops
17	394.4	29.5	1261	8	ATTHIRDB	Z23109 A.thaliana
18	390	29.2	27408	8	ATF15J1	AL117188 Arabidops
19	390	29.2	197859	8	ATCHRIV83	AL161587 Arabidops
20	335.4	25.1	1423	6	AR008096	AR008096 Sequence
21	333.8	25.0	1423	8	PCTRXB	X76119 Penicillium
22	321	24.0	2425	8	NEUCYS9	D45049 Neurospora
23	308	23.1	300425	1	AP005038	AP005038 Streptomy
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26	300.2	22.5	2592	8	SPU63713	U63713 Schizosacch
27	300.2	22.5	3058	8	AF535134	AF535134 Schizosac
28	300.2	22.5	17311	8	SPBC3P6	AL022019 S.pombe c
29	300.2	22.5	31184	8	YSCD9476	U28372 Saccharomyc
30	299.6	22.4	1898	1	SCTRXABGN	X92105 Streptomyce
31	293.2	21.9	4026	1	SC0007313	AJ007313 Streptomy
32	289	21.6	87340	1	AP005224	AP005224 Corynebact
33	283	21.2	13994	1	AE005952	AE005952 Caulobact
34	278.6	20.9	300200	1	AP005962	AP005962 Bradyrhiz
35	277.2	20.7	2134	8	SCU10274	U10274 Saccharomyc
36	275	20.6	12130	1	AE011416	AE011416 Leptospir
37	274.6	20.6	39954	8	YSCH8263	U00059 Saccharomyc
38	272.8	20.4	349841	1	BX572406	BX572406 Rhodospheu
39	267.2	20.0	210205	1	AY223810	AY223810 Rhodococc
40	265.2	19.9	963	6	AX488837	AX488837 Sequence
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# ALIGNMENTS

RESULT 1  
AK104317  
LOCUS  
DEFINITION  
Oryza sativa (japonica cultivar-group) cDNA clone.001-024-C03, full  
insert sequence.  
AK104317  
ACCESSION  
VERSION  
FLI\_CDNA; oligo capping.  
KEYWORDS  
SOURCE  
Oryza sativa (japonica cultivar-group)  
ORGANISM  
Oryza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Eriaristaceae; Oryzae; Oryza.

Pred. No. is the number of results predicted by chance to have a

Agrobiological Sciences Rice Full-Length cDNA Project Team:  
 Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K.,  
 Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, E., Hotta, I.,  
 Kojima, K., Nishiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C.,  
 Ohtsuka, K., Shishiki, T., Foundation of Advancement of International  
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 Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,  
 Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,  
 Narioka, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J.,  
 Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,  
 Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN:  
 Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,  
 Hara, A., Hashizume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,  
 Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y.,  
 Saico, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,  
 Yoshino, M., and Hayashizaki, Y.  
 Collection, mapping, and annotation of over 28,000 cDNA clones from  
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 2 (bases 1 to 1389)  
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,  
 Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W.,  
 Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hirooka, T.,  
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 Tagawa, A., Takahashi, P., Takaku-Akahira, S., Tanaka, T., Tomaru, A.,  
 Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., and  
 Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and  
 Yoshimura, A.  
 Direct Submission  
 Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of  
 Agrobiological Sciences, Department of Molecular Genetics, Head of  
 Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki  
 305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp,  
 Tel: 81-29-838-7007, Fax: 81-29-838-7007)  
 This clone is one of the 28K full-length cDNA clones from japonica  
 rice.  
 URL: <http://cdna01.dna.affrc.go.jp/cDNA/>  
 NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K.,  
 Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J.,  
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 Yamamoto, M.  
 PALS Genome Sequencing & Analysis Group: Ohtsuka, K., Iida, Y.,  
 Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,  
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 Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,  
 Yoshimura, A., Matsubara, K. and Murakami, K.  
 Genome Exploration Research Group in Riken Genomic Sciences Center  
 and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K.,  
 Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,  
 Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,  
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Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,  
 Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F.,  
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 Gaps 1;  
 QY 87 ACCTATGAGGAGATCCGCGCGCTTCCGCTCCGCAOCCGCGATCTGCATCTCGGAGCGG 146  
 DB 104 AGCCATGAGGAGATCCGCGCGCGCTCCGCAOCCGCGATCTGCATCTCGGAGCGG 163  
 QY 147 TCCCGCTCGGCACACGCGCAGCATCTAGCGCGCGCGCGCGCGCGCTCAAGCTGTGCTCTT 206  
 DB 164 GCGCTCGCGCGCACACGCGCGCGCGCTAGCGCGCGCGCGCGCGCGCTCAAGCTGTGCTCTT 223  
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 DB 224 CGAGGCTTGGCTTGGCCAAACGACATCGCGCGCGCGCGCGCGCGCTACACACCGACCGAGCT 283  
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 QY 327 CGCGAGTCCCTCGCTTGTGGCAACAATCTCTCCGAGACCGCTCAACCGCGCTCGAGCTT 386  
 DB 344 CGCCGAGTCCCTCGCTTGTGGCAACAATCTCTCCGAGACCGCTCAACCGCGCTCGAGCTT 403  
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 DB 464 GCTTCCGAGGAGGCGCTTCCGCGCGCGCTTCCGCTTCCGCGCGCTCAACCGCTCGAGCTT 523  
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TITLE  
 JOURNAL

COMMENT

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RESULT 2  
 AK071251  
 LOCUS  
 DEFINITION  
 Oryza sativa (japonica cultivar-group) cDNA clone.J023087H21, full insert sequence.  
 AK071251  
 ACCESSION  
 AK071251.1 GI:32981274  
 VERSION  
 FLI CDNA; CAP tripper.  
 KEYWORDS  
 Oryza sativa (japonica cultivar-group)  
 SOURCE  
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 ORGANISM  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

REFERENCE  
 AUTHORS  
 The Rice Full-length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-length cDNA Project Team:  
 Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yabuchi, T., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Nishikawa, T., Ohneda, E., Yabuchi, T., Suzuki, K., Li, C., Hara, A., Hashizume, W., Hayatsu, N., Imamura, K., Imotani, K., Itoh, Y., Itoh, M., Koyama, T., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.  
 Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice  
 Science 301 (5631), 376-379 (2003)

TITLE  
 JAPONICA RICE  
 JOURNAL  
 MEDLINE  
 22752273  
 PUBMED  
 12869764  
 REFERENCE  
 AUTHORS  
 2 (bases 1 to 1502)  
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Kato, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koyama, T., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, T., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M.,

Namiki, T., Narikawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Sakai, K., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sugabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.  
 Direct Submission  
 Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: shikuchi@nias.affrc.go.jp, Tel: 81-29-838-7007, Fax: 81-29-838-7007)  
 This clone is one of the 28K full-length cDNA clones from japonica rice.  
 URL: <http://cdna01.dna.affrc.go.jp/cdna/>

NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.  
 Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Kato, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koyama, T., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Ota, Y., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sugabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.

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 Best Local Similarity 80.7%; Pred. No. 3.3e-120;  
 Matches 956; Conservative 0; Mismatches 228; Indels 1; Gaps 1;

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 Qy 207 CGAGGCGCTGGATGGCGCACACGACATCCGCGCGCGGCGGAGCTCACACACCGAGCT 266  
 Db 240 CGAGGCGCTGGATGGCGCACACGACATCCGCGCGCGGCGGAGCTCACACACCGAGCT 299  
 Qy 267 CGAGGACTCCCGCGCTTCCCGACGCGGATCATGGCGCGCGGAGCTCATGAGCACTCGG 326  
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507	CGCGCGCATCTCCGCGTGGCGTCTGTACGGTGGCGGCCCCCATCTTCGCTAAACAAGCC	566
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AKI06368	AKI06368	1393 bp	mRNA	linear	PLN 24-JUL-2003
LOCUS	Oryza sativa (japonica cultivar-group)				cdna clone:002-102-C03, full
DEFINITION	insert sequence.				
ACCESSION	AKI06368				
VERSION	AKI06368.1 GI:32991577				
KEYWORDS	FLI CDNA; oligo capping.				

SOURCE ORGANISM	REFERENCE AUTHORS
1. <i>Staphylococcus aureus</i>	1. Smith, J. D. & Jones, A. B.
2. <i>Escherichia coli</i>	2. Brown, C. E. & Green, F. G.
3. <i>Salmonella typhimurium</i>	3. White, H. I. & Black, L. J.
4. <i>Pseudomonas aeruginosa</i>	4. Gray, M. K. & Hall, N. O.
5. <i>Streptococcus pneumoniae</i>	5. King, P. Q. & Lee, R. S.
6. <i>Candida albicans</i>	6. Taylor, S. T. & Adams, V. W.
7. <i>Aspergillus fumigatus</i>	7. Baker, D. U. & Miller, E. V.
8. <i>Micrococcus luteus</i>	8. Clark, G. H. & Evans, J. K.
9. <i>Bacillus subtilis</i>	9. Foster, J. L. & Wright, M. N.
10. <i>Haemophilus influenzae</i>	10. Scott, R. P. & Phillips, A. D.

## REFERENCE AUTHORS

TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS
1. The effect of the use of a computer on the performance of a task	Journal of the American Medical Association	1980;232:1000-1002	1980;232:1000-1002	1980;232:1000-1002	Smith J, Jones K
2. The effect of the use of a computer on the performance of a task	Journal of the American Medical Association	1980;232:1000-1002	1980;232:1000-1002	1980;232:1000-1002	Smith J, Jones K
3. The effect of the use of a computer on the performance of a task	Journal of the American Medical Association	1980;232:1000-1002	1980;232:1000-1002	1980;232:1000-1002	Smith J, Jones K
4. The effect of the use of a computer on the performance of a task	Journal of the American Medical Association	1980;232:1000-1002	1980;232:1000-1002	1980;232:1000-1002	Smith J, Jones K
5. The effect of the use of a computer on the performance of a task	Journal of the American Medical Association	1980;232:1000-1002	1980;232:1000-1002	1980;232:1000-1002	Smith J, Jones K
6. The effect of the use of a computer on the performance of a task	Journal of the American Medical Association	1980;232:1000-1002	1980;232:1000-1002	1980;232:1000-1002	Smith J, Jones K
7. The effect of the use of a computer on the performance of a task	Journal of the American Medical Association	1980;232:1000-1002	1980;232:1000-1002	1980;232:1000-1002	Smith J, Jones K
8. The effect of the use of a computer on the performance of a task	Journal of the American Medical Association	1980;232:1000-1002	1980;232:1000-1002	1980;232:1000-1002	Smith J, Jones K
9. The effect of the use of a computer on the performance of a task	Journal of the American Medical Association	1980;232:1000-1002	1980;232:1000-1002	1980;232:1000-1002	Smith J, Jones K
10. The effect of the use of a computer on the performance of a task	Journal of the American Medical Association	1980;232:1000-1002	1980;232:1000-1002	1980;232:1000-1002	Smith J, Jones K

TITLE  
JOURNAL

COMMENT

*Oryza sativa* (japonica cultivar-group)  
*Oryza sativa* (japonica cultivar-group)  
 Eurykaryota; Viridiplantae; Streptophyta;  
 Embryophyta; Tracheophyta;  
 Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriocarpaceae; Oryzaceae; Oryza.

The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:  
 Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Ooi, K.,  
 Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,  
 Kojima, K., Namiiki, T., Ohneda, E., Yanagi, W., Suzuki, K., Li, C.,  
 Chutskui, K., Shishiki, T., Foundation of Advancement of International  
 Science Genome Sequencing & Analysis Group: Ootomo, Y., Murakami, K.,  
 Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,  
 Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,  
 Nariakawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., NiiKura, J.,  
 Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,  
 Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN,  
 Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,  
 Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M.,  
 Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y.,  
 Sato, R., Saeki, D., Sato, K., Shibata, K., Shingawa, A., Shiraki, T.,  
 Yoshino, M. and Hayashizaki, Y.

japonica rice  
science 301 (5631), 376-379 (2003)

22752273  
12869764

2 (bases 1 to 1383)

## AUTHORS

Yamada, H., Iamamoto,  
Yoshimura, A.  
Direct Submission

Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of  
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305-8602, Japan [E-mail: skikuchi@nias.affrc.go.jp,  
tel: 03-028-0226-7007 fax: 03-028-038-7007]

This clone is one of the 28K full-length cDNA clones from japonica rice.

URL : <http://cdna01.dna.affrc.go.jp/cDNA/>

NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and Yamamoto, M.

PAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fujimura, T., Ikeda, P., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Sugiyama, A., Narikawa, R., Nishikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xi, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.  
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,



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## ORIGIN

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LOCUS
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BAC clone:OJ1479_B12, complete sequence.
ACCESSION
AP004165
VERSION
AP004165.2 GI:34447188
KEYWORDS
HTG
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriarthoideae; Oryzaceae; Oryza.
REFERENCE
1
AUTHORS
Sasaki, T., Matsumoto, T. and Yamamoto, K.
TITLE
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC
clone:OJ1479_B12
JOURNAL
Published Only in Database (2001)
REFERENCE
2 (bases 1 to 118300)
AUTHORS
Sasaki, T., Matsumoto, T. and Yamamoto, K.
TITLE
Direct Submission
JOURNAL
Submitted (12-SEP-2001) Takuji Sasaki, National Institute of
Agricultural Sciences, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail: tsasaki@nias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/,
Tel: 81-298-38-7441, Fax: 81-298-38-7468)
COMMENT
On Sep 3, 2003 this sequence version replaced gi:15594177.
The orientation of the sequence is from M13rev to -21M13 of the BAC
clone. The nucleotide sequence of this BAC clone was generated by
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ORIGIN
Query Match      53.1%; Score 709.6; DB 8; Length 118300;
Best Local Similarity 85.1%; Pred. No. 1.4e-104;
Matches 793; Conservative 0; Mismatches 139; Indels 0; Gaps 0;

QY 87 AGCTATGAGGAGTCCCGCGCTCCGCTCCGCAACCGCATCTGCATTCGCGAGCGG 146
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 Qy 567 CATCGCGCTCATAGCGGCGGCGGCTTCGCTGCTGAGCGTTCGCGGCGGCTTCGCTGAAACG 626  
 Db 99330 CATCGCGCTCATAGCGGCGGCGGCTTCGCTGCTGAGCGTTCGCGGCGGCTTCGCTGAAACG 99271  
 Qy 627 CGGCTCCGCTCATAGCGGCGGCGGCTTCGCTGCTGAGCGTTCGCGGCGGCTTCGCTGAAACG 686  
 Db 99270 CGGCTCCGCTCATAGCGGCGGCGGCTTCGCTGCTGAGCGTTCGCGGCGGCTTCGCTGAAACG 99211  
 Qy 687 GGCAGGCGCTTCGAGACCGCGGCGGCTTCGCTGCTGAGCGTTCGCGGCGGCTTCGCTGAAACG 746  
 Db 99210 GGCAGGCGCTTCGAGACCGCGGCGGCTTCGCTGCTGAGCGTTCGCGGCGGCTTCGCTGAAACG 99151  
 Qy 747 CTATGCGGCGGCGGCGGCGGCTTCGCTGCTGAGCGTTCGCGGCGGCTTCGCTGAAACG 806  
 Db 99150 CTATGCGGCGGCGGCGGCGGCTTCGCTGCTGAGCGTTCGCGGCGGCTTCGCTGAAACG 99091  
 Qy 807 TGAGGCTTCGAGACCGCGGCGGCTTCGCTGCTGAGCGTTCGCGGCGGCTTCGCTGAAACG 866  
 Db 99090 TGAGGCTTCGAGACCGCGGCGGCTTCGCTGCTGAGCGTTCGCGGCGGCTTCGCTGAAACG 99031  
 Qy 867 CAAATTCCTGGGCGGCGGCGGCTTCGCTGCTGAGCGTTCGCGGCGGCTTCGCTGAAACG 926  
 Db 99030 CAAATTCCTGGGCGGCGGCGGCTTCGCTGCTGAGCGTTCGCGGCGGCTTCGCTGAAACG 98971  
 Qy 927 TTCACATCAGCAGGCTTCGAGACCGCGGCGGCTTCGCTGCTGAGCGTTCGCGGCGGCTTCGCTGAAACG 986  
 Db 98970 TTCACATCAGCAGGCTTCGAGACCGCGGCGGCTTCGCTGCTGAGCGTTCGCGGCGGCTTCGCTGAAACG 98911  
 Qy 987 CCGTCAGGCGCTTACTGCGCGCTGGATCAGGTT 1018  
 Db 98910 TCGCAGGCTTACTGCGCGCTGGATCAGGTT 98879

RESULT 6  
 AX366999  
 LOCUS 1560 bp DNA linear PAT 16-FEB-2002  
 DEFINITION Sequence 26 from Patent WO0198509.  
 ACCESSION AX366999  
 VERSION AX366999.1 GI:18698275  
 KEYWORDS  
 SOURCE Oryza sativa  
 ORGANISM Oryza sativa  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzoideae; Oryza.  
 REFERENCE 1  
 Lanahan, M.B., Desai, N.M. and Gasdaska, P.Y.  
 Authors Grain processing method and transgenic plants useful therein  
 Title Patent: WO 0198509-A 26 27-DEC-2001;  
 Journal Syngenta Participations AG (CH)  
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 ORIGIN  
 Query Match 53.0%; Score 708; DB 6; Length 1560;  
 Best Local Similarity 85.0%; Pred. No. 4.1e-104;

Matches 792; Conservative 0; Mismatches 140; Indels 0; Gaps 0;  
 Qy 87 AGCTATGAGGAGTCCGCGCGCTCCGCTCCGACGCGCATCTGATCATTCGCGAGCGG 146  
 Db 402 AGCATGAGGAGTCCGCGCGCTCCGCTCCGACGCGCTGATCATTCGCGAGCGG 461  
 Qy 147 TCCGCTGCGGACACGCGGCGCTTACGCGGCGCGCGGCGGCTCAAGCTGCTGCTTT 206  
 Db 462 GCGCTGCGGCGGACACGCGGCGCTTACGCGGCGCGCGGCGGCTCAAGCTGCTGCTTT 521  
 Qy 207 CGAGGCTGCGGACACGCGGCGCTTACGCGGCGCGCGGCGGCTCAAGCTGCTGCTTT 266  
 Db 522 CGAGGCTGCGGACACGCGGCGCTTACGCGGCGCGCGGCGGCTCAAGCTGCTGCTTT 581  
 Qy 267 CGAGGCTGCGGACACGCGGCGCTTACGCGGCGCGCGGCGGCTCAAGCTGCTGCTTT 326  
 Db 582 CGAGGCTGCGGACACGCGGCGCTTACGCGGCGCGCGGCGGCTCAAGCTGCTGCTTT 641  
 Qy 327 CGGCGCTGCGGACACGCGGCGCTTACGCGGCGCGCGGCGGCTCAAGCTGCTGCTTT 386  
 Db 642 CGGCGCTGCGGACACGCGGCGCTTACGCGGCGCGCGGCGGCTCAAGCTGCTGCTTT 701  
 Qy 387 TTGCGCTGCGGACACGCGGCGCTTACGCGGCGCGCGGCGGCTCAAGCTGCTGCTTT 446  
 Db 702 TTGCGCTGCGGACACGCGGCGCTTACGCGGCGCGCGGCGGCTCAAGCTGCTGCTTT 761  
 Qy 447 CGTTCGCGGAGCGGCGGCGCTTACGCGGCGCGCGGCGGCTCAAGCTGCTGCTTT 506  
 Db 762 CGTTCGCGGAGCGGCGGCGCTTACGCGGCGCGCGGCGGCTCAAGCTGCTGCTTT 821  
 Qy 507 CGGCGCTGCGGACACGCGGCGCTTACGCGGCGCGCGGCGGCTCAAGCTGCTGCTTT 566  
 Db 822 CGGCGCTGCGGACACGCGGCGCTTACGCGGCGCGCGGCGGCTCAAGCTGCTGCTTT 881  
 Qy 567 CATCGCGCTCATAGGCGGCGGCGCTTACGCGGCGCGCGGCGGCTCAAGCTGCTGCTTT 626  
 Db 882 CATCGCGCTCATAGGCGGCGGCGCTTACGCGGCGCGCGGCGGCTCAAGCTGCTGCTTT 941  
 Qy 627 CGGCTGCGGACACGCGGCGCTTACGCGGCGCGCGGCGGCTCAAGCTGCTGCTTT 686  
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 Db 1002 GGCAGGCGGCTTACGCGGCGGCGCTTACGCGGCGCGCGGCGGCTCAAGCTGCTGCTTT 1061  
 Qy 747 CTATGCGGCGGCGGCGGCGCTTACGCGGCGGCGGCGGCTCAAGCTGCTGCTTT 806  
 Db 1062 CTATGCGGCGGCGGCGGCGCTTACGCGGCGGCGGCGGCTCAAGCTGCTGCTTT 1121  
 Qy 807 TGAGGCTTCCGAGTCTTACGCGGCGGCGCTTACGCGGCGGCGGCGGCTCAAGCTGCTGCTTT 866  
 Db 1122 TGAGGCTTCCGAGTCTTACGCGGCGGCGCTTACGCGGCGGCGGCGGCTCAAGCTGCTGCTTT 1181  
 Qy 867 CAAATTCCTGGGCGGCGGCGGCTTACGCGGCGGCGGCGGCTCAAGCTGCTGCTTT 926  
 Db 1182 CAAATTCCTGGGCGGCGGCGGCTTACGCGGCGGCGGCGGCTCAAGCTGCTGCTTT 1241  
 Qy 927 TTCCACTCAGCAGGCTTACGCGGCGGCGCTTACGCGGCGGCGGCGGCTCAAGCTGCTGCTTT 986  
 Db 1242 TTCCACTCAGCAGGCTTACGCGGCGGCGCTTACGCGGCGGCGGCGGCTCAAGCTGCTGCTTT 1301  
 Qy 987 CCGTCAGGCGCTTACTGCGCGCTGGATCAGGTT 1018  
 Db 1302 TCGCAGGCTTACTGCGCGCTGGATCAGGTT 1333

RESULT 7  
 AX654214  
 LOCUS 1130 bp DNA linear PAT 22-MAR-2003  
 DEFINITION Sequence 4084 from Patent WO03000898.  
 ACCESSION AX654214  
 VERSION AX654214.1 GI:29157028

DB 785 GCGTCCGTGGCGCGGCTCAAGAACTGTGTGACGCCGCGAGGTCTTCGCAGCCTCC 844

QY 824 AGTGTCCTGGCTCTTTCTTCGCCATTCGGCATGGCATGAGCCGCGACCACAAATTCTTGGCGGCGAC 883

DB 845 AGTGTCCTGGCTCTTTCTTCGCCATTCGGCATGGCATGAGCCGCGACCACAAATTCTTGGCGGCGG 904

QY 884 ACCTTGAATCGCATTCAGATGATGATGTGTGTAAGAACCAAGCCAGGTTCCTCATCACACAGTG 943

DB 905 AGCTCGAGCTGACTCCGATGCTATGTGTGTCACCAAGCCCGGCTCCAATCACACACAGCG 964

QY 944 TAAAGGGTGATTTGTCGTCTGGCAGCTGCAGGACAAGAAGTACCGTCAGGCCAATTAATCTG 1003

DB 965 TCAGGGAGTCTTCGCGCGCGGTGATGTTTCAGGACAGAGATATCGCAGGCCAATTAATCTG 1024

QY 1004 CCGCTGATCAGGGTGCATGGCTGCATGG 1033

DB 1025 CGCGGGATCAGATCGAAGACCTTCACAG 1054

RESULT 8  
AP005477  
LOCUS  
DEFINITION  
ORyza sativa (japonica cultivar-group) chromosome 6 clone  
OSUNB0039F24, \*\*\* SEQUENCING IN PROGRESS \*\*\*,  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

HTG: HTGS PHASE2.  
Oriza sativa (japonica cultivar-group)  
Oriza sativa (japonica cultivar-group)  
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;  
Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae;  
Eriartoideae; Oryzaceae; Oryza.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Sasaki, T., Matsumoto, T. and Katayose, Y.  
Oriza sativa nipponbare (GA3) genomic DNA, chromosome 6, BAC  
clone: OSJNBb0039F24  
Published Only in Database (2002)  
2 (bases 1 to 131980)  
Sasaki, T., Matsumoto, T. and Katayose, Y.  
Direct Submission  
Submitted (26-JUN-2002) Takuji Sasaki, National Institute of  
Agrobiological Sciences, Rice Genome Research Program, Kannondai  
2-1-2, Tsukuba, Ibaraki 305-8602, Japan  
(E-mail: tsasaiken@affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/,  
Tel: 81-298-38-7441, Fax: 81-298-38-7468)  
NOTE: It currently consists of 1 contigs. Gaps between the contigs  
are represented as runs of N. The order of the pieces is believed  
to be correct as given, however the sizes of the gaps between them  
are based on estimates that have provided by the submitter. This  
sequence will be replaced by the finished sequence as soon as it is  
available and the accession number will be preserved.  
\* NOTE: This is a 'working draft' sequence.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.

FEATURES  
source  
location/Qualifiers  
1. 131980  
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ORIGIN  
  
Query Match 51.2%; Score 683.4; DB 2; Length 131980;  
Best Local Similarity 81.4%; Pred. No. 2.2e-100;  
Matches 792; Conservative 0; Mismatches 181; Indels 0; Gaps 0;

QY 44 CCACCGCGCGCGCGCGCAAGCCAGCCAACTGATGAGCGCTATGAGGAGGATCCG 103

104 CCAGCGCTCCGCTCCGACGCGCATCTGCATCATCGGAGCGGTCCGCTGCGCACACGG 163  
164 CAGCATCTACGCGCCCGCGCGGAGCTCAAGCTCTGCTCTTCGAGGCGTGCATGCCA 223  
2706 CGCGGCTCTACGCGCGCGCGCGGAGCTCAAGCGGTCTCTTCGAGGCTTCTCGCCA 82765  
224 ACAGCATCGCGCGCGCGCGGAGCTCAACACACCGACGCGTGCAGAACTTCCCGGCT 283  
2766 ACAGCATCGCGCGCGCGGAGCTCAACACACCGACGCGTGCAGAACTTCCCGGCT 82825  
284 TCCCAACCGCATCATGCGCGCGCATCTCATGAGCAATCGCGCGCGCATCTCGGCT 343  
2826 TCCCAACCGCATCTCTCGCGCGCGCATCTCATGAGCAATCGCGCGCGCATCTCGGCT 82885  
344 TTGCGACCAATCTCTCTCGAGACGCTCAACCGCGCTCTCTTCGCGCTGCGCATTC 403  
2886 TCGGACACAGATCTCTCAACGAGACGCTCAACCGCGCTCTCTTCGCGCTGCGCATTC 82945  
404 GAGTACTGAGACTCTCCACACCGCTCTCTCGCGAGCGGTATGTTGCGACGCGGACCG 463  
2946 GCGTGCCTCTCGCGCACACCGCTCTCTCGAGCGGCTCTCTTCGCGCTGCGCATTC 83005  
464 TCGCGCGCGCTCTCTCTCGCGCGCTCTCTCGAGCGGCTCTCTTCGCGCTGCGCATTC 523  
3006 TCGCGCGCGCTCTCTCTCGCGCGCTCTCTCGAGCGGCTCTCTTCGCGCTGCGCATTC 83065  
524 GTGCGCTCTGAGCGGTCTCGCGCGCTCTCTCGAGCGGCTCTCTTCGCGCTGCGCATTC 583  
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584 GCGCGCTCTGAGCGGTCTCGCGCGCTCTCTCGAGCGGCTCTCTTCGCGCTGCGCATTC 643  
3126 GCGCGCTCTGAGCGGTCTCGCGCGCTCTCTCGAGCGGCTCTCTTCGCGCTGCGCATTC 83185  
644 TCATCCACCGCGCAATCTCTCGCGCTCTCTCGAGCGGCTCTCTTCGCGCTGCGCATTC 703  
3186 TCATCCACCGCGCAATCTCTCGCGCTCTCTCGAGCGGCTCTCTTCGCGCTGCGCATTC 83245  
704 ACCCGCAATTAAGTCTCTGAGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCTCTGAG 763  
3246 ACCCGCAATTAAGTCTCTGAGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCTCTGAG 83305  
764 GCGCGCTCTGAGCGGTCTGAGCGGTCTGAGCGGTCTGAGCGGTCTGAGCGGTCTGAG 823  
3306 GCGGTCTCTGAGCGGTCTGAGCGGTCTGAGCGGTCTGAGCGGTCTGAGCGGTCTGAG 83365  
824 AGGTCTCTGAGCGGTCTGAGCGGTCTGAGCGGTCTGAGCGGTCTGAGCGGTCTGAG 883  
3366 AGGTCTCTGAGCGGTCTGAGCGGTCTGAGCGGTCTGAGCGGTCTGAGCGGTCTGAG 83425  
884 AGGTCTCTGAGCGGTCTGAGCGGTCTGAGCGGTCTGAGCGGTCTGAGCGGTCTGAG 943  
3426 AGGTCTCTGAGCGGTCTGAGCGGTCTGAGCGGTCTGAGCGGTCTGAGCGGTCTGAG 83485  
944 TAAAGGTCTGAGCGGTCTGAGCGGTCTGAGCGGTCTGAGCGGTCTGAGCGGTCTGAG 1003  
3486 TCAAGGTCTGAGCGGTCTGAGCGGTCTGAGCGGTCTGAGCGGTCTGAGCGGTCTGAG 83455  
1004 CCGTCTGATCAGG 1016  
3546 CCGTCTGATCAGG 83558

RESULT 9  
AX653785  
LOCUS AX653785 963 bp DNA linear PAT 22-MAR-2003  
DEFINITION Sequence 3655 from Patent WO03000898.  
ACCESSION AX653785  
VERSION AX653785.1 GI:29156599  
KEYWORDS  
SOURCE Oryza sativa

ORGANISM Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.  
REFERENCE 1  
AUTHORS Chang, H. S., Chen, W., Cooper, B., Glazebrook, J., Goff, S. A., Hou, Y. M.,  
Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.  
TITLE Plant genes involved in defense against pathogens  
JOURNAL Patent: WO 03000898-A 3655 03-JAN-2003;  
SYNOPSIS Syngenta Participations AG (CH)  
FEATURES  
Location/Qualifiers  
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Query Match 46.7%; Score 623.4; DB 6; Length 963;  
Best Local Similarity 81.0%; Pred. No. 1.7e-90;  
Matches 754; Conservative 0; Mismatches 141; Indels 36; Gaps 1;  
1 ATGAGGAGATCG 150  
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151 GCTGCGCACACG 210  
61 TCGGCGCACACG 120  
211 GGTGAGATCG 270  
121 GGTGAGATCG 180  
271 AGCTTCCCG 330  
181 AGCTTCCCG 240  
331 AGCTTCCCG 390  
241 AGCTTCCCG 300  
391 AGCTTCCCG 450  
301 AGCTTCCCG 360  
451 AGCTTCCCG 510  
361 AGCTTCCCG 420  
511 AGCTTCCCG 570  
421 AGCTTCCCG 480  
571 AGCTTCCCG 630  
481 AGCTTCCCG 540  
631 AGCTTCCCG 690  
541 AGCTTCCCG 600  
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661 AGCTTCCCG 684  
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685 AGCTTCCCG 744

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QY 871 TTCTGGCGGACAGCTTGAACCTCGATTCAGATCGTTATGTGGAACCAAGCCAGGTTC 930
Db 745 TTTCTGGCGGACAGCTTGAACCTCGATTCAGATCGTTATGTGGAACCAAGCCAGGTTC 804
QY 931 ACTCACACAGCTGTAAAGGTGTATTGTGCTGCTGGGACGTGACGACAGAGTACCT 990
Db 805 ACCGACACAGCTGTAAAGGTGTATTGTGCTGCTGGGACGTGACGACAGAGTATCGC 864
QY 991 CAGGCCATTACTGCCGCTGGATCAGGCTGCA 1021
Db 865 CAGGCTATTACTGCCGCTGGATCAGAGATCA 895

RESULT 10
AX366997
LOCUS 1021 bp DNA linear PAT 16-FEB-2002
DEFINITION Sequence 24 from Patent WO0198509.
ACCESSION AX366997
VERSION AX366997.1 GI:18698274
KEYWORDS
SOURCE
ORGANISM Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
REFERENCE
AUTHORS Lanan,M.B., Desai,N.M. and Gasdaska,P.Y.
TITLE Grain processing method and transgenic plants useful therein
JOURNAL Patent: WO 0198509-A 24 27-DEC-2001;
Syngenta Participations AG (CH)
FEATURES
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ORIGIN
Query Match 42.1%; Score 562.8; DB 6; Length 1021;
Best Local Similarity 74.2%; Pred. No. 9e-81;
Matches 730; Conservative 0; Mismatches 242; Indels 12; Gaps 1;

QY 113 CGTTCGCGACGCGATCTGATCATATCGGAGCGGTCCGCTGGCGACACGGAGCATCT 172
Db 26 CTCACACACCGCGCTCTGATCGCTTGCTGCTCCGCGCGGTGCGCCACACCGCGCCATCT 85
QY 173 ACGCGCGCGCGGAGCTCAAGCTCTGCTCTTCGAGGCTGTGATGGCCACAGCATCG 232
Db 86 ACGCGCGCGCGGAGCTCAAGCTCTGCTCTTCGAGGCTGTGATGGCCACAGCATCG 145
QY 233 CCGCGCGCGGCGAGCTCACACACACACACACCTGCGAGAACTTCCCGGGCTTCCCAAG 292
Db 146 CCGCGCGCGGCGAGCTCACACACACACACACCTGCGAGAACTTCCCGGGCTTCCCGAGG 205
QY 293 GCATCATGGGCGCGACCTCATAGACCACTGCGCGCGGAGTCCCTGCGTTTGGCACCA 352
Db 206 GCATCTCGCGGTGGAGCTACCGACAACTTCCGCAAGAGGAGCGCTTCGGCACCA 285
QY 353 ACATCTCTCCGAGACCTCACCGCTCCGCTTTCGCGCTGCCATTCGCGAGTTAGTG 412
Db 266 CCATCTTCAGGAGACCTGACCAAGGTGACCTTCGAGCAAGCGCTTCAAGCTCTTCA 325
QY 413 CAGACTCCACAA CGTCTCTCGCGATCGGTTATCGTTGCCAGGGAGCGCTTCGCGGC 472
Db 326 CCGACTCCAAAGGCCATCTTCGCGACCGCGTGTCTCTGCGCATCGCGCGCTGGCCAAAGT 385
QY 473 GCTTCCACTTCCCGGGTC-----CGATGCATACTGCAACCGCGGATCTTCGG 520
Db 386 GGCTCTCTCTGCTGGGTCTCGCGGAGGTGCTCGCGGCTCTGGACCGGGGATCTCGG 445
QY 521 CCGTGGCGGCTGTGACGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 580
Db 446 CCGTGGCTGTGTGCGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 505
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QY 581 GCGGCGGCGACTCCGCTATGAGAGAGTCCAAATTTCTCTACCAAGTACGGCTCCAGCTCT 640
Db 506 GTGCGGAGACAGCGCGATGAGAGAGGCGCAACTTCTCTACCAAGTACGGCTCCAGAGTCT 565
QY 641 ACATCATCCACGCGCGCAATACCTTTCCGTGCTTCCAGATCATGAGGCGCGCGGCTTG 700
Db 566 ACATCATCCACGCGCGCGAGCTTCCGCGCTTCCAGATCATGAGGCGCGCGCTCT 625
QY 701 AGAAGCCCAAAATTAAAGTCTCTCGGACTCGGAAGTTGTTCAGGCTTATGCGGCGCAA 760
Db 626 CCAAGCCGAAGATCGACGCTCATCTGAACTCTCCGTGCTGAGGCTTACGCGCGAGCGG 685
QY 761 ACGGCGGCCCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 820
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QY 821 TTCAAGGTGCTGCGCTCTTTTCGCGCATGCGGCTAGCGTGTGACCGCGGAGCTTCCGAC 880
Db 746 TCAAGGTGCTGCGGCTCTTTTCGCGCATGCGGCTAGCGTGTGACCGCGGAGCTTCCGAC 805
QY 881 GACAGCTTGAACCTCGATTCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 940
Db 806 GCGGCTGAGCTGAGCTTCCGCGCTAGCGTGTGACCGAGCGCGGCGACCAACCGACCT 865
QY 941 GTGTAAGGCTGTATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1000
Db 866 CCGTGCCTGGCTGTTCGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 925
QY 1001 CTGCGCTGAGTACGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1060
Db 926 CCGCGCGCGCGCACCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 985
QY 1061 GTGCAAGGAGGGAAGTCTGATT 1084
Db 986 GTCCGAGCGGCGGAGTCCGACT 1009

RESULT 11
AX507791
LOCUS 1152 bp DNA linear PAT 27-SEP-2002
DEFINITION Sequence 2486 from Patent WO0216655.
ACCESSION AX507791
VERSION AX507791.1 GI:23389028
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
REFERENCE
AUTHORS Harper,J.F., Kreps,J., Wang,X. and Zhu,T.
TITLE Stress-regulated genes of plants, transgenic plants containing
same, and methods of use
JOURNAL Patent: WO 0216655-A 2486 28-FEB-2002;
The Scripps Research Institute (US); Syngenta Participations AG
(CH)
FEATURES
Location/Qualifiers
source
1..1152
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/mol_type="unassigned DNA"
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ORIGIN
Query Match 34.2%; Score 457; DB 6; Length 1152;
Best Local Similarity 67.9%; Pred. No. 8.8e-64;
Matches 659; Conservative 0; Mismatches 300; Indels 12; Gaps 1;

QY 128 TCTGATCATCGGAGCGGTCCGCTGCGCACACGCGAGCCATCTACGCGGCGCGCG 187
Db 182 TTTGATCTCGGAGTGGACCGAGCAGCACACACGCGCGGCTATGATCATCGAGAGCG 241
QY 188 AGCTAAGCTGTGCTCTTCGAGGCGCTGATGCGCAAGCATCGCGCGGCGGCGACG 247
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Db 242 AGCTTAAGCCTCTCTCTTCGAGGATGGATGCTTAACGACATCGCTCCGCGCGGTCAAT 301  
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Db 302 TACTACACACACGACGCTCGAGAACTTCCGCGGCTTCCCAACGCAATCATGCGCGCG 361  
QY 308 ACTCATGAGCAACTCCGCGCGCGAGTCCGCGGCTTCCCAACGCAATCATGCGCGCG 367  
Db 362 ATATCGCTGAGAAATTCAGAAACAAATCGAGAGATTCGAACTACGATCTTCACGAA 421  
QY 368 CGCTACCGCGCGCGAGTTCGCGGCTTCCCAACGCAATCATGCGCGCGCGTCAAT 427  
Db 422 CTGTTCACAAAGTGTATCTCTCATGAAACCGTTTAAGCTATTCAGTATTCAGAACTG 481  
QY 428 TCCTCGCGAGTGTATGCTGTCGAGGAGCGCTTCGCGGCGCGCTTCACGCGCGCG 487  
Db 482 TCTCGCGTGTATCTGTAATCATCTTCTGAGGAGCTGTTGCTAAACGCTTCTAGCTT 541  
QY 488 GGTCCGATGCA-----TACTGGAACCGCGGCAATCTCCGCGCGCGCGTGTG 535  
Db 542 GATCTGTTGAGGTAATGCTGCTGTTTGGAACTGCTGATCTCCGCTTGTGCTTGG 601  
QY 536 ACGTTCGCGCGCGCGAGTTCGCGGCGCGCGCTTCGCGGCGCGCGTCAAT 595  
Db 602 ACGAGCTGCTCGGATTTTGAAGATTAAGCTTCTTGTGCTTGTGCTTGTGCTTGT 661  
QY 596 CTATGAGGAGTCCAAATTTCTCAGCAAGTACGGCTCCGCGCGCGCGTCAAT 655  
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QY 656 GCAATACCTTCGCTGCTTCCAAAGATCATGAGCGCGCGCGCTTGAAGACCCCAATTA 715  
Db 1082 GGTGATGCGCGCGAGTGTGATGAGAGCATTTATTAAGAGATTTGATCTCAGAGGGTA 1141  
QY 1076 AGTCTGATGCA 1086  
Db 1142 AGAGTATGCA 1152

RESULT 12  
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LOCUS AX651358 1152 bp DNA linear PAT 22-MAR-2003  
DEFINITION Sequence 148 from Patent WO03000898.  
ACCESSION AX651358  
VERSION AX651358.1 GI:29154176  
KEYWORDS  
SOURCE Arabidopsis thaliana (thale cress)  
ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source

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## ORIGIN

Query Match \ 34.2%; Score 457; DB 6; Length 1152;  
Best Local Similarity 67.9%; Pred. No. 8.8e-64;  
Matches 659; Conservative 0; Mismatches 300; Indels 12; Gaps 1;  
QY 128 TCTGATCATCGGAGCGGTCCGCTGCGCACACGCGGCGGCTTACGCGCGCGCGCG 187  
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

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Chang, H. S., Chen, W., Cooper, B., Glazebrook, J., Goff, S. A., Hou, Y. M.,  
Karagiri, F., Qian, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.  
Plant genes involved in defense against pathogens  
Patent: WO 03000898-A 148 03-JAN-2003;  
Syngenta Participations AG (CH)  
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RESULT 13

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LOCUS Arabidopsis thaliana clone RAFL16-02-L06 (RS0174) putative

DEFINITION thiorodoxin reductase (NADPH) 2 (At4g35460) mRNA, complete cds.

ACCESSION BT004322.1 GI:28393818

VERSION 1

KEYWORDS F11 CDNA.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 1433)

AUTHORS Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Kawai,J., Kim,C.J., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

TITLE Arabidopsis Full Length cDNA Clones

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1433)

AUTHORS Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Kawai,J., Kim,C.J., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

TITLE Direct Submission

JOURNAL Submitted (14-FEB-2003) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA

COMMENT RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

THE Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada,K., Chan,M.M., Chang,C.H., Dale,J.M., Hsuan,V.W., Lee,J.M., Chodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yu,G., Yuan,S., Chen,H., Cheuk,R., Jones,T., Kim,C.J., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Tripp,M.G., Wu,T., Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.

Annotation based on July 2002 version of the Arabidopsis genome submitted to Genbank

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3'UTR

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ACCESSION 223108  
VERSION 223108.1 GI:468523  
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SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
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1 (bases 1 to 1148)  
JACQUOT, J.P., RIVERA-MADRIG, R., MARINHO, P., KOLLAROVA, M., LE  
MARECHAL, P., MIGINIAC-MASLOW, M. and MEYER, Y.  
Arabidopsis thaliana NADPH thioredoxin reductase. cDNA  
characterization and expression of the recombinant protein in  
Escherichia coli  
J. Mol. Biol. 235 (4), 1357-1363 (1994)

JOURNAL MEDLINE  
PUBMED 8308900  
REFERENCE 2 (bases 1 to 1148)  
Meyer, Y.  
Direct Submission  
Submitted (24-JUN-1993) Yves Meyer, Labo de Physio et Biol Mol  
Végétales, CNRS, URA 565, Av. de Villeneuve, PERPIGNAN, 66860,  
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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747736

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Genesec\_29Jan04.\*

1: Genesecq1980s.\*

2: Genesecq1990s.\*

3: Genesecq2000s.\*

4: Genesecq2001as.\*

5: Genesecq2001bs.\*

6: Genesecq2002s.\*

7: Genesecq2003as.\*

8: Genesecq2003bs.\*

9: Genesecq2003cs.\*

10: Genesecq2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	757.6	56.7	1391	3 AAC62460	AAC62460 Barley NA
2	708	53.0	1560	6 AAD29838	AAD29838 Rice NADP
3	684.4	51.2	1130	7 ADA70761	ADA70761 Rice gene
4	623.4	46.7	963	7 ADA70332	ADA70332 Rice gene
5	562.8	42.1	1021	6 AAD29837	AAD29837 Arabidops
6	457	34.2	1152	3 AAC43307	AAC43307 Arabidops
7	457	34.2	1152	6 ABZ14681	ABZ14681 Arabidops
8	457	34.2	1152	7 ADA67905	ADA67905 Arabidops
9	457	34.2	1152	3 AAC48213	AAC48213 Arabidops
10	440.6	33.0	6357	7 AAL54488	AAL54488 Thioresox
11	440.6	33.0	6357	9 AAD26526	AAD26526 Thalecres
12	435.8	32.6	6357	7 AAL54493	AAL54493 Thioresox
13	435.8	32.6	6357	9 AAD26531	AAD26531 Thalecres
14	435.8	32.6	6357	9 AAD26533	AAD26533 Thalecres
15	434.6	32.5	1313	3 AAC34825	AAC34825 Arabidops
16	434.2	32.5	6357	7 AAL54494	AAL54494 Thioresox
17	434.2	32.5	6357	7 AAL54490	AAL54490 Thioresox
18	434.2	32.5	6357	9 AAD26528	AAD26528 Thalecres
19	434.2	32.5	6357	9 AAD26532	AAD26532 Thalecres
20	433.8	32.5	1375	3 AAC38745	AAC38745 Arabidops
21	432.8	32.4	1458	3 AAC38830	AAC38830 Arabidops
22	432.8	32.4	1539	3 AAC36511	AAC36511 Arabidops
23	432.8	32.4	1540	3 AAC51123	AAC51123 Arabidops

24	432.6	32.4	6357	7 AAL54484	AAL54484 Thioresox
25	432.6	32.4	6357	7 AAL54492	AAL54492 Thioresox
26	432.6	32.4	6357	7 AAL54485	AAL54485 Thioresox
27	432.6	32.4	6357	9 ADD26530	ADD26530 Thalecres
28	432.6	32.4	6357	9 ADD26522	ADD26522 Thalecres
29	432.6	32.4	6357	9 ADD26523	ADD26523 Thalecres
30	431.8	32.3	3787	6 ABN89582	ABN89582 Phaseolin
31	431.8	32.3	3787	6 ABS53098	ABS53098 cDNA enco
32	431.8	32.3	4546	6 ABN89583	ABN89583 Phaseolin
33	431.8	32.3	4546	6 ABS53099	ABS53099 DNA encod
34	431	32.3	6356	9 ADD26529	ADD26529 Thalecres
35	431	32.3	6357	7 AAL54491	AAL54491 Thioresox
36	431	32.3	6357	7 AAL54480	AAL54480 Thioresox
37	431	32.3	6357	7 AAL54489	AAL54489 Thioresox
38	431	32.3	6357	7 AAL54487	AAL54487 Thioresox
39	431	32.3	6357	9 ADD26525	ADD26525 Thalecres
40	431	32.3	6357	9 ADD26518	ADD26518 Thalecres
41	431	32.3	6357	9 ADD26517	ADD26517 Thalecres
42	431	32.3	6357	9 ADD26534	ADD26534 Thalecres
43	431	32.3	6357	9 ADD26527	ADD26527 Thalecres
44	431	32.3	6408	7 AAL54482	AAL54482 Thioresox
45	430.8	32.2	4545	6 ABN89584	ABN89584 Phaseolin

ALIGNMENTS

RESULT 1

AAC62460 AAC62460 standard; DNA; 1991 BP.

AC AAC62460;

DT 07-FEB-2001 (first entry)

DE Barley NADPH-thioredoxin reductase coding sequence.

XX Barley; NADPH-thioredoxin reductase; disulfide bridge reduction; NTR; development; thioredoxin h; hair care product; venom neutralisation; food technology; food allergy; ds.

OS Hordeum vulgare.

PN WO200058352-A2.

PD 05-OCT-2000.

PF 31-MAR-2000; 2000WO-US008566.

PR 31-MAR-1999; 99US-0127198P.

PR 06-DEC-1999; 99US-0169162P.

PR 21-JAN-2000; 2000US-0177739P.

XX 21-JAN-2000; 2000US-0177740P.

(REGC ) UNIV CALIFORNIA.

PI Cho M, Del Val G, Caillaud M, Lemaux PG, Buchanan BB;

WPI: 2000-679291/66.

P-PSDB; AAB29250.

XX Recombinant or isolated nucleic acid, useful for producing transgenic plants with altered redox properties, encode thioredoxin h or thioredoxin reductase.

PS Claim 66; Fig 5B; 125pp; English.

CC The present invention relates to the isolation and use of the barley thioredoxin h and NADPH-thioredoxin reductase coding and protein sequences. Thioredoxin is thought to be involved in plant development via its function in the reduction of disulfide bridges. Thioredoxin can be used in hair care products and in the neutralisation of some venoms and toxins, and is also useful in the reduction of some food, for example it

CC can be used to reduce the allergenicity of foods and the digestibility of  
CC some proteins. It can also be used to enhance the baking qualities of  
CC cereal flour

SQ Sequence 1991 BP; 338 A; 675 C; 591 G; 368 T; 0 U; 19 Other;

Query Match 56.7%; Score 757.6; DB 3; Length 1991;  
Best Local Similarity 84.4%; Pred. No. 8.9e-163;  
Matches 841; Conservative 0; Mismatches 155; Indels 0; Gaps 0;

QY 91 ATGAGGATCCCGCGCGCTCGCTCCGACGCGCATCTGCGAGCGATCTGCGAGCGGATCC 150  
DB 996 ATGAGGATCCCGCGCGCGCTCGCTCCGACGCGCATCTGCGAGCGGATCCCGCGCG 1055  
QY 151 GCTGCGACAGCGAGCATCTAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 210  
DB 1056 GNCGCGCACAGCGCGCGCATCTAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1115  
QY 211 GGTGATGCGCAACGACATCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 270  
DB 1116 GGTGATGCGCAACGACATCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1175  
QY 271 AACTCCCGCGCTTCCCAACGCGCATCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 330  
DB 1176 AACTCCCGCGCTTCCCAACGCGCATCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1235  
QY 331 CAGTCCCTCGCGCTTGGACCAACATCTCTCGAGACCGTCCACCGCGCGCGCGCGCG 390  
DB 1236 CAGTCCCTCGCGCTTGGACCAACATCTCTCGAGACCGTCCACCGCGCGCGCGCGCG 1295  
QY 391 GCTTCCCGCGCTTCCCAACGCGCATCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 450  
DB 1296 GCGCGCGCTTCCCAACGCGCATCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1355  
QY 451 GCGAGCG 510  
DB 1356 GCGAGCG 1415  
QY 511 GGCATCTCCGCGCTTGGACCAACATCTCTCGAGACCGTCCACCGCGCGCGCGCGCG 570  
DB 1416 GGCATCTCCGCGCTTGGACCAACATCTCTCGAGACCGTCCACCGCGCGCGCGCGCG 1475  
QY 571 GCGGTCTAGCG 630  
DB 1476 GCGGCG 1535  
QY 631 TCCACGCTCTACATCATCTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 690  
DB 1536 TCCACGCTCTACATCATCTCCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1595  
QY 691 AGCGCGCTTGAACCG 750  
DB 1596 AGCGCGCTTGAACCG 1655  
QY 751 GCG 810  
DB 1656 GCGCGCTTGAACCG 1715  
QY 811 GTCTCGGATCTTACGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 870  
DB 1716 GTCTCGGATCTTACGCTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1775  
QY 871 TTCTCGGCG 930  
DB 1776 TTCTCGGCG 1835  
QY 931 ACTCACACCGAGTGAAGGCTGATTTCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 990  
DB 1836 ACATACACCGAGTGAAGGCTGATTTCTGCTGCGCGCGCGCGCGCGCGCGCGCGCGCG 1895  
QY 991 CAGGCGATCTTACGCTTGGATCGAGGCTGATTTCTGCTGCGCGCGCGCGCGCGCGCG 1050  
DB 1896 CAGGCGATCTTACGCTTGGATCGAGGCTGATTTCTGCTGCGCGCGCGCGCGCGCGCG 1955

QY 1051 CAGGAGATCGGTGCACAGGAGGGAAGTCTGATTGA 1086  
DB 1956 NAGGAGGTGGGTGCANAGGTGNCAGTCTGATTGA 1991

## RESULT 2

AAD29838  
ID AAD29838 standard; DNA; 1560 BP.

XX AAD29838;

AC AC

DT 17-MAY-2002 (first entry)

XX Rice NADPH dependent thioredoxin reductase DNA (NTR).

XX Transgenic plant; thioredoxin reductase; starch; protein; grain;

XX milling process; enzyme; rice; ds.

OS Oryza sativa.

XX Key Location/Qualifiers

FT CDS 406..1338

FT /\*tag= a

FT /product= "Rice NTR"

XX W0200198509-A2.

XX 27-DEC-2001.

XX 19-JUN-2001; 2001WO-EP006918.

XX 21-JUN-2000; 2000US-00599747.

XX (SYGN ) SYNGENTA PARTICIPATIONS AG.

XX Lanahan MB, Desai NM, Gasdaska PY;

XX WPI; 2002-179557/23.

XX P-PSDB; AAE18733.

XX Transgenic plant coding for eukaryotic thioredoxin reductase at elevated

XX levels useful for separating the starch and protein components of grain

XX in a milling process.

XX Claim 12; Page 81; 86pp; English.

XX The present invention relates to a transgenic plant comprising

XX heterologous DNA coding for eukaryotic thioredoxin reductase integrated

XX into its nuclear or plastid genome and use of thioredoxin reductase for

XX separating the starch and protein components of grain in a milling

XX process. Transgenic plant is used for separating the starch and protein

XX components of grain in a milling process. Transgenic plant may be used to

XX produce thioredoxin reductase at elevated levels. Delivery of thioredoxin

XX reductase eliminates the need to develop exogenous sources for addition

XX during processing. Secondly, physical disruption of seed integrity is not

XX necessary to bring the enzyme in contact with the storage or matrix

XX proteins of the seed prior to processing or as an extra processing step.

XX The present sequence is rice NADPH dependent thioredoxin reductase DNA

XX (NTR)

XX SQ Sequence 1560 BP; 302 A; 435 C; 439 G; 372 T; 0 U; 12 Other;

Query Match 53.0%; Score 708; DB 6; Length 1560;

Best Local Similarity 85.0%; Pred. No. 1.7e-151;

Matches 792; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

QY 87 AGCTATGAGGATCCCGCGCGCTCGCTCCGACGCGCATCTGCGAGCGG 146

DB 402 AGCCATGAGGATCCCGCGCGCTCGCTCCGACGCGCATCTGCGAGCGG 461

QY 147 TCCCGTCTGCGCACACGCGCAGCCATCTTACGCGCGCGCGCGCGCGCTCAAGCCTGTGCTCTT 206

Db 462 GCCGTGGGCGACACGGGGGGATCTAGCGCGCGCGGGAGCTCAAGCCGCTCTT 521  
Qy 207 CGAGGGTGGATGCCCAACGACATCGCGGGGGGGGAGCTCAACCAACCAACGAGT 266  
Db 522 CGAGGGTGGCTCGCAAGACATCGCGGGGGGGGAGCTCAACCAACCAACGAGT 581  
Qy 267 CGAGAACTTCGGGGCTTCCCAAGCGACATCGCGGGGGGGGAGCTCAACCAACCAACGAGT 326  
Db 582 CGAGAACTTCGGGGCTTCCCAAGCGAGATCTCGCGGGGGGGGAGCTCAACCAACCAACGAGT 641  
Qy 327 CGCGAGTTCCTCGCGCTTGGGACCAACATCTCTCGGAGACCGCTCAACCGCGCTCGACTT 386  
Db 642 CGCGAGTTCCTCGCGCTTGGGACCAACATCTCTCGGAGACCGCTCAACCGCGCTCGACTT 701  
Qy 387 TTGGGCTGCGCCATTCGAGTTAGTGAGATTCACAAACCGTCTCGCGGATGGGTAT 446  
Db 702 CTGCGCGCGCGCTTCCGCTCGCTCGAGTCCAGCAACCGTCTCGCGGAGCGGCTCGT 761  
Qy 447 CGTTGCCAAGCGAGCGCGCGGCTCCACTTCCCGGGGCGGATCGATGATCACTGAA 506  
Db 762 CGTGCACACCGCGCGCTCGCGGGGAGTCCACTTTCGCGGGCTCGAGCGCTACTGAA 821  
Qy 507 CGCGGATTCCTCGCTGCTGTGAGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 566  
Db 822 CGCGGATTCCTCGCTGCTGTGAGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 881  
Qy 567 CATCGCGCTATAGCGCGGAGTCCGCTATGAGGAGTCCATTTCTTCCCAAGTA 626  
Db 882 CATCGCGCTATAGCGCGGAGTCCGCTATGAGGAGTCCATTTCTTCCCAAGTA 941  
Qy 627 CGGTTCACATCATCATCCCGCGCGCAATCTTCCGTCTTCCAAAGTATGCA 686  
Db 942 CGGTTCACATCATCATCCCGCGCGCAACACTTCCCGCGCGCGCGCGCGCGCGCGCG 1001  
Qy 687 GCGCAGGCGCTTGGAAACCCCAAAATTAAGTCTCTGGAAGTCTGGAAGTCTGAGGC 745  
Db 1002 GCGCAGGCGCTTGGAAACCCCAAGATCCAGTCTTCTGGAAGTCTGGAAGTCTGAGGC 1061  
Qy 747 CTATGGCGCGCAACCG 806  
Db 1062 CTACGGCGCGGAGGTGAGGTGCAATGGCTGGTCTGAGTGAAGTCTGAGTCTGAGT 1121  
Qy 807 TGAGTCTCGATCTTCAAGTCTTGGGCTCTTCTTCCGCAATCGGCGATGAGCGCGAC 866  
Db 1122 GAAGATCTCGACCTTCAAGTCTTGGGCTCTTCTTCCGCAATCGGCGATGAGCGCGAC 1181  
Qy 867 CAATTCCTGCGCGGACAGCTTGAAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 926  
Db 1182 GAAGTCTCTGCGCGGCGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 1241  
Qy 927 TTCCACTCACAACGAGTGAAGGAGTATTTGCTGCTGCGCAAGTGAAGGAGTGAAGTA 986  
Db 1242 CTCCAGCACAACGAGTGAAGGAGTCTTCTGCTGCTGCGGATGTCAGGAGTGAAGTA 1301  
Qy 987 CGGTGAGGCGATTAAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 1018  
Db 1302 TCGCGCGCTTACTGCGCGTGAAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGT 1333

## RESULT 3

ADA70761

ID ADA70761 standard, DNA; 1130 BP.

XX

AC ADA70761;

XX

DT 20-NOV-2003 (first entry)

XX

DE Rice gene, SEQ ID 4084.

XX

KW Plant; bacterial infection; fungal infection; viral infection; rice;

XX

RW gene; ds.

XX

OS Oryza sativa.

XX FN WO2003000898-A1.  
XX PD 03-JAN-2003.  
XX PP 22-JUN-2001; 2001WO-IB001105.  
XX PR 22-JUN-2001; 2001WO-IB001105.  
XX PA (SYN ) SYNGENTA PARTICIPATIONS AG.  
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;  
XX Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;  
XX WPI; 2003-175290/17.  
DR Identifying at least one gene involved in plant resistance or response to  
XX pathogenic infection for conferring resistance or tolerance to a plant to  
XX bacterial, fungal or viral infection by determining or detecting plant  
XX gene expression.  
XX Claim 6; SEQ ID NO 4084; 899pp; English.  
XX The present invention relates to a method (M1) for identifying genes  
XX involved in plant resistance or response to pathogenic infection. M1  
XX comprises identifying a gene whose expression is significantly altered in  
XX the incompatible interaction of plant gene expression relative to  
XX expression of the gene in an uninfected plant, in a mutant plant that  
XX does not express a gene associated with response to pathogenic infection,  
XX or in a corresponding incompatible or compatible interaction. (M1) is  
XX useful for conferring resistance to resistance or tolerance to a plant to  
XX bacterial, fungal or viral infection. The present sequence was used to  
XX illustrate the invention.  
SQ Sequence 1130 BP; 174 A; 419 C; 358 G; 179 T; 0 U; 0 Other;

Query Match 51.2%; Score 684.4; DB 7; Length 1130;  
Best Local Similarity 80.7%; Pred. No. 3.7e-146;  
Matches 799; Conservative 0; Mismatches 191; Indels 0; Gaps 0;  
Qy 44 CCACCG 103  
Db 65 CGCGCGCGTTCGGGTTCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 124  
Qy 104 CGCGCGCTCGCTTCG 163  
Db 125 CG 184  
Qy 164 CAGCATCTACCG 223  
Db 185 CGCGCGCTTCAGCG 244  
Qy 224 ACACATCG 283  
Db 245 ACACATCG 304  
Qy 284 TCCCAACG 343  
Db 305 TCCCAACG 364  
Qy 344 TTGGCACCAATCTCTTCGCGAGACCGTCAACCGCGCGCGCGCGCGCGCGCGCGCG 403  
Db 365 TCGGACCGAGTCTTCAACCGAGACCGTCAACCGCGCGCGCGCGCGCGCGCGCGCG 424  
Qy 404 GAGTAGTGAGACTCCAGACCGTCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 463  
Db 425 GCGTCGCGCTTCG 484  
Qy 464 TCG 523  
Db 485 TCG 544  
Qy 524 GTGCGCGCTCTGAGCGGTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 583



DB 545 GGGCGGCTGCGACGGCGCGCGCCCATCTTCGGAACAAGCCCATGCGCGTCTCGCG 604  
QY 584 GGGCGGCTGCGACGGCGCGCGCCCATCTTCGGAACAAGCCCATGCGCGTCTCGCG 643  
DB 605 GGGCGGCTGCGACGGCGCGCGCCCATCTTCGGAACAAGCCCATGCGCGTCTCGCG 664  
QY 644 TCATCACCGCGCAATACCTTCGCGTCTTCGGAACAAGCCCATGCGCGTCTCGCG 703  
DB 665 TCATCACCGCGCAATACCTTCGCGTCTTCGGAACAAGCCCATGCGCGTCTCGCG 724  
QY 704 ACCCAAAATTAAGTCTCTCGGACTCGGAAGTGTGCGAGCCCTATGCGCGCGCAACG 763  
DB 725 ACCCAAAATTAAGTCTCTCGGACTCGGAAGTGTGCGAGCCCTATGCGCGCGCAACG 784  
QY 764 GGGCGGCTGCGACGGCGCGCGCCCATCTTCGGAACAAGCCCATGCGCGTCTCGCG 823  
DB 785 GGGCGGCTGCGACGGCGCGCGCCCATCTTCGGAACAAGCCCATGCGCGTCTCGCG 844  
QY 824 AGGTGCTGCGGCTCTCTTCGCGATCGGCGCATGCGCGCGCAACGCGCGCGCAACG 883  
DB 845 AGGTGCTGCGGCTCTCTTCGCGATCGGCGCATGCGCGCGCAACGCGCGCGCAACG 904  
QY 884 AGCTTGAATCGAATTCAGATGTTATGCGGAACCAAGCCGATTCCTACCTACCAAGT 943  
DB 905 AGCTGAGCTGAGTCCGATGCTATGCTGACCAAGCCGCTCCACTCACACGCG 964  
QY 944 TAAAGGCTGATTTGCTGCGGCTGCGAGTGCAGGCAAGGACCTGCGAGGCTTACTG 1003  
DB 965 TCAAGGAGTCTTCGCGCGCGGCTGATGTTGAGGCAAGGATTCGCGAGGCTTACTG 1024  
QY 1004 CGCTGATCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1033  
DB 1025 CGCGGATCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1054

RESULT 4  
ID ADA70332 standard; DNA; 963 BP.  
AC ADA70332;  
DT 20-NOV-2003 (first entry)  
DE Rice gene, SEQ ID 3655.  
KW Plant; bacterial infection; fungal infection; viral infection; rice;  
KW gene; ds.  
OS Oryza sativa.  
PN W0200300898-A1.  
XX 03-JAN-2003.  
XX 22-JUN-2001; 2001NO-15001105.  
XX 22-JUN-2001; 2001NO-15001105.  
XX (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;  
XX Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;  
XX WPI; 2003-175290/17.  
XX Identifying at least one gene involved in plant resistance or response to  
XX pathogenic infection for conferring resistance or tolerance to a plant to  
XX bacterial, fungal or viral infection by determining or detecting plant  
XX gene expression.  
XX Claim 6; SEQ ID NO 3655; 899pp; English.

CC The present invention relates to a method (M1) for identifying genes  
CC involved in plant resistance or response to pathogenic infection. M1  
CC comprises identifying a gene whose expression is significantly altered in  
CC the incompatible interaction of plant gene expression relative to  
CC the incompatible interaction of plant gene expression relative to  
CC expression of the gene in an uninfected plant, in a mutant plant that  
CC does not express a gene associated with response to pathogenic infection,  
CC or in a corresponding incompatible or compatible interaction. (M1) is  
CC useful for conferring resistance to resistance or tolerance to a plant to  
CC bacterial, fungal or viral infection. The present sequence was used to  
CC illustrate the invention.  
XX  
SQ Sequence 963 BP; 159 A; 334 C; 292 G; 178 T; 0 U; 0 Other;  
Query Match 46.7%; Score 623.4; DB 7; Length 963;  
Best Local Similarity 81.0%; Pred. No. 2.9e-132;  
Matches 754; Conservative 0; Mismatches 141; Indels 36; Gaps 1;  
QY 91 ATGAGGAGATCCGCGCGCTCCGCTCGCGCGCATCTGCTCATCGGAGCGGTC 150  
DB 1 ATGAGGAGATCCGCGCGCTCCGCTCGCGCGCATCTGCTCATCGGAGCGGTC 60  
QY 151 GCTGCGCACAGCGCGCATCTGCTCGCGCGCGCGCGCATCTGCTCATCGGAG 210  
DB 61 TCGGCGCACAGCGCGCATCTGCTCGCGCGCGCGCGCATCTGCTCATCGGAG 120  
QY 211 GCTGCGCACAGCGCGCATCTGCTCGCGCGCGCGCGCATCTGCTCATCGGAG 270  
DB 121 GCTGCGCACAGCGCGCATCTGCTCGCGCGCGCGCGCATCTGCTCATCGGAG 180  
QY 271 AACTTCCCGGCTTCCGCGCGCATCTGCTCGCGCGCGCGCATCTGCTCATCGGAG 330  
DB 181 AACTTCCCGGCTTCCGCGCGCATCTGCTCGCGCGCGCGCATCTGCTCATCGGAG 240  
QY 331 CAGTCCCTCGGCTTCCGCGCGCATCTGCTCGCGCGCGCGCATCTGCTCATCGGAG 390  
DB 241 CAGTCCCTCGGCTTCCGCGCGCATCTGCTCGCGCGCGCGCATCTGCTCATCGGAG 300  
QY 391 GCTGCGCACAGCGCGCATCTGCTCGCGCGCGCGCATCTGCTCATCGGAG 450  
DB 301 GCTGCGCACAGCGCGCATCTGCTCGCGCGCGCGCATCTGCTCATCGGAG 360  
QY 451 GCTGCGCACAGCGCGCATCTGCTCGCGCGCGCGCATCTGCTCATCGGAG 510  
DB 361 GCTGCGCACAGCGCGCATCTGCTCGCGCGCGCGCATCTGCTCATCGGAG 420  
QY 511 GCTGCGCACAGCGCGCATCTGCTCGCGCGCGCGCATCTGCTCATCGGAG 570  
DB 421 GCTGCGCACAGCGCGCATCTGCTCGCGCGCGCGCATCTGCTCATCGGAG 480  
QY 571 GCTGCGCACAGCGCGCATCTGCTCGCGCGCGCGCATCTGCTCATCGGAG 630  
DB 481 GCTGCGCACAGCGCGCATCTGCTCGCGCGCGCGCATCTGCTCATCGGAG 540  
QY 631 TCCGAGCTTACATCATCCAGCGCGCGCATCTGCTCGCGCGCGCGCATCTGCTCATCGGAG 690  
DB 541 TCCGAGCTTACATCATCCAGCGCGCGCATCTGCTCGCGCGCGCGCATCTGCTCATCGGAG 600  
QY 691 AGGCGGCTTACATCATCCAGCGCGCGCATCTGCTCGCGCGCGCGCATCTGCTCATCGGAG 750  
DB 601 AGGCGGCTTACATCATCCAGCGCGCGCATCTGCTCGCGCGCGCGCATCTGCTCATCGGAG 660  
QY 751 GCGCGCGCAAGCGCGCGCATCTGCTCGCGCGCGCGCATCTGCTCATCGGAG 810  
DB 661 GCGCGCGCAAGCGCGCGCATCTGCTCGCGCGCGCGCATCTGCTCATCGGAG 684  
QY 811 GCTGCGCACAGCGCGCATCTGCTCGCGCGCGCGCATCTGCTCATCGGAG 870  
DB 685 GCGCGGCTTACATCATCCAGCGCGCGCATCTGCTCGCGCGCGCGCATCTGCTCATCGGAG 744  
QY 871 TCCGAGCTTACATCATCCAGCGCGCGCATCTGCTCGCGCGCGCGCATCTGCTCATCGGAG 930  
DB 745 TTTCTCGCGCGCAAGCGCGCGCATCTGCTCGCGCGCGCGCATCTGCTCATCGGAG 804



QY 931 ACTCACACCAAGTGTAAAGGTGTATTGCTGTGGGACCTGCAGGACAAAGATACCTT 990  
 DB 805 ACGCACACCAAGTGTAAAGGTGTATTGCTGTGGGACCTGCAGGACAAAGATACCTC 864  
 QY 991 CAGGCCATTACTGCGCTGGATCAGGGTGCA 1021  
 DB 865 CAGGCTATTACTGCGCTGGATCAGGATCA 895

RESULT 5  
 AAD29837  
 ID AAD29837 standard; DNA; 1021 BP.  
 XX  
 AC AAD29837;  
 XX  
 DT 17-MAY-2002 (first entry)  
 XX  
 DE Arabidopsis NADPH dependent thioredoxin reductase DNA (NTR).  
 XX  
 KW Transgenic plant; thioredoxin reductase; starch; protein; grain;  
 KW milling process; enzyme; ds.  
 XX  
 OS Arabidopsis sp.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 10..1011  
 FT /\*tag= a  
 FT /product= "Arabidopsis NTR"  
 XX  
 PW W0200198509-A2.  
 XX  
 PD 27-DEC-2001.  
 XX  
 PF 19-JUN-2001; 2001WO-EP006918.  
 XX  
 PR 21-JUN-2000; 2000US-00598747.  
 XX  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 XX  
 PI Lanahan MB, Desai NM, Gasdaska PY;  
 XX  
 DR NPI; 2002-179557/23.  
 DR P-PSDB; AAE18732.  
 XX  
 PT Transgenic plant coding for eukaryotic thioredoxin reductase at elevated  
 PT levels useful for separating the starch and protein components of grain  
 PT in a milling process.  
 XX  
 PS Claim 12; Page 79; 86pp; English.

The present invention relates to a transgenic plant comprising heterologous DNA coding for eukaryotic thioredoxin reductase integrated into its nuclear or plastid genome and use of thioredoxin reductase for separating the starch and protein components of grain in a milling process. Transgenic plant is used for separating the starch and protein components of grain in a milling process. Transgenic plant may be used to produce thioredoxin reductase at elevated levels. Delivery of thioredoxin reductase eliminates the need to develop exogenous sources for addition during processing. Secondly, physical disruption of seed integrity is not necessary to bring the enzyme in contact with the storage or matrix proteins of the seed prior to processing or as an extra processing step. The present sequence is Arabidopsis NADPH dependent thioredoxin reductase DNA (NTR)

Query Match 42.1%; Score 562.8; DB 6; Length 1021;  
 Best Local Similarity 74.2%; Pred. No. 1.9e-118;  
 Matches 730; Conservative 0; Mismatches 242; Indels 12; Gaps 1;  
 QY 113 CGTCCGACGCGCATCTGCATCATCGGAGCGTCCCGTCCGACACGCGGCGCATCT 172  
 DB 26 CTCACAAACCCCGCTCTGCATCTGTTGGCTCCGGCCCGGCTGCCACACCCCGCGCATCT 85

QY 173 ACGCGGCGCGCGGAGCTCAAGCTGTGCTCTTCGAGGGCTGGATGGCCAAAGACATCG 232  
 DB 86 ACGCGGCGCGCGGAGCTCAAGCTGTGCTCTTCGAGGGCTGGATGGCCAAAGACATCG 145  
 QY 233 CCGGCGGCGCGGAGCTCAAGCTGTGCTCTTCGAGGGCTGGATGGCCAAAGACATCG 292  
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 QY 293 GCATCATGCGCGCGGAGCTCAAGCTGTGCTCTTCGAGGGCTGGATGGCCAAAGACATCG 352  
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 QY 353 ACATCTCTCTCGAGAGCGCTCAAGCTGTGCTCTTCGAGGGCTGGATGGCCAAAGACATCG 412  
 DB 266 CCATCTCTCAAGAGAGCGCTCAAGCTGTGCTCTTCGAGGGCTGGATGGCCAAAGACATCG 325  
 QY 413 CAGATCTCAAGAGAGCGCTCAAGCTGTGCTCTTCGAGGGCTGGATGGCCAAAGACATCG 472  
 DB 326 CCGATCTCAAGAGAGCGCTCAAGCTGTGCTCTTCGAGGGCTGGATGGCCAAAGACATCG 385  
 QY 473 GCCTTCATCTCCCGGCTC-----CGATGCACTGTGAGACCGCGGCTCTCCG 520  
 DB 386 GGCTCTCTCTGCTGGGCTCCGGGAGGTGCTCGCGGCTCTCGAAACCGCGGATCTCCG 445  
 QY 521 CTTGTGCGCTGTGTGAGCGGTGCGGCGGCTCTTCGAGGGCTGGATGGCCAAAGACATCG 580  
 DB 446 CTTGTGCGCTGTGTGAGCGGTGCGGCGGCTCTTCGAGGGCTGGATGGCCAAAGACATCG 505  
 QY 581 CGGCGGCGGCTGTGTGAGCGGTGCGGCGGCTCTTCGAGGGCTGGATGGCCAAAGACATCG 640  
 DB 506 GTGGCGGAGAGCAGCGGAGGTGCGGCGGCTCTTCGAGGGCTGGATGGCCAAAGACATCG 565  
 QY 641 ACATCATCCACCGCGGCTCTTCGAGGGCTGGATGGCCAAAGACATCGAGGCGCGCTTG 700  
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 QY 701 AGAACCCCAAAATTAAGTCTCTGAGAGCTCGGAGTGTGTGAGGCTGTATGGCGGCGCAA 760  
 DB 626 CCAACCCCAAAATTAAGTCTCTGAGAGCTCGGAGTGTGTGAGGCTGTATGGCGGCGCAA 685  
 QY 761 ACGCGCGGCGGCTGTGTGAGAGCTCGGAGTGTGTGAGGCTGTATGGCGGCGCAA 820  
 DB 686 AGCGCGAGCTGTGTGAGAGCTCGGAGTGTGTGAGGCTGTATGGCGGCGCAA 745  
 QY 821 TTGAGTGTGTGAGCTGTGTGAGAGCTCGGAGTGTGTGAGGCTGTATGGCGGCGCAA 880  
 DB 746 TCAAGTGTGTGAGCTGTGTGAGAGCTCGGAGTGTGTGAGGCTGTATGGCGGCGCAA 805  
 QY 881 GACAGCTTGAATCGATTCAGATGTGTGAGAGCTCGGAGTGTGTGAGGCTGTATGGCGGCGCAA 940  
 DB 806 GCGGCGTGTGAGCTGTGTGAGAGCTCGGAGTGTGTGAGGCTGTATGGCGGCGCAA 865  
 QY 941 GTGTAAAGGTGTATTGCTGTGTGAGAGCTCGGAGTGTGTGAGGCTGTATGGCGGCGCAA 1000  
 DB 866 CCGTGTGTGAGCTGTGTGAGAGCTCGGAGTGTGTGAGGCTGTATGGCGGCGCAA 925  
 QY 1001 CTGCGCTGTGATCAGGCTGTGTGAGAGCTCGGAGTGTGTGAGGCTGTATGGCGGCGCAA 1060  
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 QY 1061 GTGCACAGGCGGAAAGTCTGATT 1084  
 DB 986 GTTCCAGGAGGAAAGTCTGACT 1009

RESULT 6  
 AAC43307  
 ID AAC43307 standard; DNA; 1152 BP.  
 XX AAC43307;  
 XX  
 DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 38790.  
XX KM Hybridisation assay; genetic mapping; gene expression control;  
XX KW protein identification; signal transduction pathway; metabolic pathway;  
XX KW Promoter; termination sequence; ss.  
XX OS Arabidopsis thaliana.  
XX PN EP1033405-A2.  
XX PD 06-SEP-2000.  
XX PF 25-FEB-2000; 2000EP-00301439.  
XX PR 25-FEB-1999; 99US-0121825P.  
XX PR 05-MAR-1999; 99US-0123180P.  
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XX (SRI ) SRIIPPS RES INST.  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX Harper JF, Xreps J, Wang X, Zhu T;  
PI  
XX WPI; 2002-304127/34.  
XX  
XX Identifying a stress condition to which a plant cell has been exposed and  
PT producing plants with increased tolerance to these abiotic stresses.  
PT  
XX Claim 14; SEQ ID NO 2486; 577pp + Sequence Listing; English.  
XX  
XX The invention relates to identifying a stress condition to which a plant  
CC cell has been exposed, comprising: (a) contacting nucleic acid  
CC representative of expressed polynucleotides in the plant cell with an  
CC array or probes representative of the plant cell genome; and (b)  
CC detecting a profile of expressed polynucleotides in the plant cell  
CC characteristic of a stress response. The method is useful in the  
CC production of transgenic plants, cells and seeds and in producing plants  
CC with increased tolerance to abiotic stress. The present sequence is that  
CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used  
CC in methods of the invention. Note: The sequence data for this patent is  
CC not represented in the printed specification but is based on sequence  
CC information supplied to Derwent by the European Patent Office  
XX  
XX Sequence 1152 BP; 281 A; 222 C; 308 G; 341 T; 0 U; 0 Other;  
SQ  
Query Match 34.2%; Score 457; DB 6; Length 1152;  
Best Local Similarity 67.9%; Pred. No. 2.5e-94;  
Matches 659; Conservative 0; Mismatches 300; Indels 12; Gaps 1;  
QY 128 TCTGCTATCTGGAGCGTCCCGCTGGCCACGCGAGCCATCTAGCGCGCGCGCG 187  
DB 182 TTTGCTATCTGGAGCGTCCCGCTGGCCACGCGAGCCATCTAGCGCGCGCGCG 241  
QY 188 AGCTCAAGCTGTCTCTTCGAGGCGCTGGAGCGCAACGAGCATCGCGCGCGCGCG 247  
DB 242 AGCTTAGCTCTTCTCTTCGAGGAGTGTGCTACGAGCATCGCTCCCGCGCGTCAAT 301  
QY 248 TCACACACACCGAGCTCGAGAACTTCGCGCGCTCCCGCAACGAGCATCTAGCGCGCG 307  
DB 302 TAACTACAAACCGAGCTCGAGAACTTCCTCGCGTCCCGTGAAGGATTTCTCGGATTG 361  
QY 308 ACCCTAGGACCACTCGCGCGCGAGCTCCCTCGCTTGGCCACCAACATCTCTCCGAGA 367  
DB 362 ATATGCTTGAGAAATTCAGAAACATTCGAGAGATTGGAACTCTTCAAGGAA 421  
QY 368 CCGTCAACCGCTGACCTTTTCGCGCTCCCGCAATTCGAGATTAGTGCAGACTCCACACCG 427  
DB 422 CTGTTTAAACAAAGTTGATTTCTCATCGAAACCGTTTAAGCTATTCACTGATTTCGAGAACTG 481  
QY 428 TCCTGCGGATCGGCTATCGTTCGAGGAGCGCTCGCGCGCGCTCCACTTCCCG 487  
DB 482 TTCCTGCTGATCTGTAATCATTTCTACTGAGCGTGTCTTAAGCTTTAGCTTTCACTG 541  
QY 488 GTCCGATGCA-----TACTGGACCGCGCATCTCCGCTGTCGCGCTGTG 535  
DB 542 GATCTGGTGAAGTAATGCTGTTTGGAAATCGGTATCTCCGCTTGTGCTGTTGCG 601  
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DB 602 ACGGAGCTGCTCCGATTTTGAAGATAAGCTCTTGTGTTATTGCTGTGTTGATTTCAG 661  
QY 596 CTATGAGGAGTCCCAATTTCTCCCAAGTAGCGCTCCGCTCACTATCAATCCACGCC 655  
DB 662 CTATGAGGAGGAGTAATTTCTGACTAAGTAGTATGATCTAAGGTTTATATTATTCATAGA 721  
QY 656 GCAATACCTTCGCTGCTCCAGAGTATCGAGCGCGCGCTTCAGAACCCCAATTA 715  
DB 722 GGGATACGTTTAGGGCGCTTAAGATTTATGACAGAGAGCTTTGTCTAACCCCTAGATTG 781  
QY 716 AGTCTCTCTGGGACTCGGAAGTTGTGAGGCGCTATGCGCGCGCAACCGCGCCCATTTGG 775

DB 782 AAGTGATTGGAACTCTCCCGTGGTGGCGGTATGGTGATGAATAATGACGTGTCTTG 841  
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DB 842 GAGGATTGAGGTGAAGATGTTGTTACTGGGAGTTTTCAGATCTGAAGGTGTCTGGAT 901  
QY 836 TCTTCTTCCCATTCGGCATGAGCCGGCGGACCAAAATTCCTGGCGGACAGCTTGAACCTG 895  
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QY 896 ATTCTAGATGTTTATGTTGAAACCAAGCCAGGTTTCCACTCACACCGAGTGTAAAGGTTAT 955  
DB 962 ATGAGATGTTTATGTTGACCAAGCCAGCTTACTTAAGACGAGCGTGTGTTGTTAT 1021  
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QY 1016 GGTGATGCTGCTCATTTGGAAGCTGAGCACTACTGCGAGGATCGGTGCAAGGAGGAA 1075  
DB 1082 GGTGATGCTGCGAGTGTGATGAGGAGCTTACTTACAGAGATTGGATCTCAGGAGGGA 1141  
QY 1076 AGTCTGATTGA 1086  
DB 1142 AGAGTATTGA 1152  
RESULT 8  
ADA67905 standard; DNA; 1152 BP.  
XX  
AC ADA67905;  
XX  
DT 20-NOV-2003 (first entry)  
XX  
DE Arabidopsis thaliana gene, SEQ ID 148.  
XX  
KW Plant; bacterial infection; fungal infection; viral infection; ds.  
XX  
OS Arabidopsis thaliana.  
XX  
PN W02003000898-A1.  
XX  
PD 03-JAN-2003.  
XX  
PF 22-JUN-2001; 2001WO-IB001105.  
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PR 22-JUN-2001; 2001WO-IB001105.  
XX  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;  
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;  
XX  
DR WPI; 2003-175290/17.  
XX  
XX Identifying at least one gene involved in plant resistance or response to  
PT pathogenic infection for conferring resistance or tolerance to a plant to  
PT bacterial, fungal or viral infection by determining or detecting plant  
PT gene expression.  
XX  
PS Claim 6; SEQ ID NO 148; 899pp; English.  
XX  
CC The present invention relates to a method (M1) for identifying genes  
CC involved in plant resistance or response to pathogenic infection. M1  
CC comprises identifying a gene whose expression is significantly altered in  
CC the incompatible interaction of plant gene expression relative to  
CC expression of the gene in an uninfected plant, in a mutant plant that  
CC does not express a gene associated with response to pathogenic infection,  
CC or in a corresponding incompatible or compatible interaction. (M1) is  
CC useful for conferring resistance to resistance or tolerance to a plant to  
CC bacterial, fungal or viral infection. The present sequence was used to



PR	18-JUN-1999;	99US-0139455P.
PR	18-JUN-1999;	99US-0139456P.
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PR	04-OCT-1999;	99US-0157117P.
PR	05-OCT-1999;	99US-0157753P.
PR	06-OCT-1999;	99US-0157865P.
PR	07-OCT-1999;	99US-0158029P.
PR	08-OCT-1999;	99US-0158232P.
PR	12-OCT-1999;	99US-0158369P.
PR	13-OCT-1999;	99US-0159293P.
PR	13-OCT-1999;	99US-0159294P.
PR	13-OCT-1999;	99US-0159295P.
PR	14-OCT-1999;	99US-0159329P.
PR	14-OCT-1999;	99US-0159330P.
PR	14-OCT-1999;	99US-0159331P.
PR	14-OCT-1999;	99US-0159637P.
PR	18-OCT-1999;	99US-0159584P.
PR	21-OCT-1999;	99US-0160741P.
PR	21-OCT-1999;	99US-0160767P.
PR	21-OCT-1999;	99US-0160768P.
PR	21-OCT-1999;	99US-0160770P.
PR	21-OCT-1999;	99US-0160814P.
PR	22-OCT-1999;	99US-0160815P.
PR	22-OCT-1999;	99US-0160980P.
PR	22-OCT-1999;	99US-0160981P.
PR	22-OCT-1999;	99US-0160989P.
PR	25-OCT-1999;	99US-0161404P.
PR	25-OCT-1999;	99US-0161405P.
PR	25-OCT-1999;	99US-0161406P.
PR	26-OCT-1999;	99US-0161359P.
PR	26-OCT-1999;	99US-0161360P.
PR	28-OCT-1999;	99US-0161361P.
PR	28-OCT-1999;	99US-0161920P.
PR	28-OCT-1999;	99US-0161992P.
PR	28-OCT-1999;	99US-0161993P.
PR	29-OCT-1999;	99US-0162142P.

Query Match 34.2%; Score 457; DB 3; Length 1375;  
Best Local Similarity 67.9%; Freq. No. 2.6e-94; Mismatches 0; Indels 12; Gaps 1;  
Matches 659; Conservative

Qy	128	TCTGTCATCATCGGAGCGGTCCCGCTGGCCACACGCGAGCCATCTACGGGCGCGCGG	187
Db	171	TTTGTCATCGTGGAGTGGACACACACGCGCGGATCTATGTCATCGAGAGCGG	230
Qy	188	AGCTAAGCCTGTCTTTCGAGGGTGGATGCCAACGACATCGCGGGCGGCGAGC	247
Db	231	AGCTTAAGCCTCTTCTTCGAGAGGATGGATGGCTAACGACATCGTCCCGCGGCTCAAT	290

QY 248 TCACCAACACCGACGTCGAGAACTTCCCGGGCTTCCCAACGGGATCAGGCGCGC 307  
Db 291 TAACTACAAACACCGACGTCGAGAACTTCCCGGGCTTCCCAACGGGATCAGGCGCGC 350  
QY 308 ACCTCATGGAACACTGCGCGGCGGCTTCCCGGGCTTCCCAACGGGATCAGGCGCGC 367  
Db 351 ATATCGTTGAGAAATTCAGAAACAAATCGGAGAGATTTGGAACTACGATCTTCACGGAA 410  
QY 368 CCGTCACCGCGGTCGACCTTTTCGGCGCTGCCCACTTCGAGTTAGTGCAGACTCCCAACCG 427  
Db 411 CTGTAAACAAAGTTGATTTCTCATCGAAACCGTTTAAAGCTATTCACGATTCGAGACTG 470  
QY 428 TCCTCGCGAGTGGTTATCGTTGCGACGGAGCGGCTGCGGGGCGCTCCACTTCCCGC 487  
Db 471 TTCTCGCTGATCTGTAATCATTTCTACTGAGAGCTGTGCTAAAGCTTTAGCTTCACTG 530  
QY 488 GGTGCGATGCA-----TACTGGAACCGCGGATCTCCCGCTCTGCGCTGCTGTG 535  
Db 531 GATCTGTTGAGGTAATGTTGCTTTTGGATCGTGTATCTCCGCTTGTGCTGTTGCG 590  
QY 536 ACGTGGCGGCGGCTTCCCGGTAACAGCGGCTGCGGGGCGGCTCCACTTCCCGC 595  
Db 591 ACGGAGCTGCTCCGATTTTGGAGTAAGGCTTGTGCTGTTATGCTGCTGCTGCTGCTG 650  
QY 596 CTATGAGGAGTCCAAATTTCTCACCAGTACGGCTCCCGCTTACATCATCCACGCGC 655  
Db 651 CTATGAGGAGTCCAAATTTCTCACCAGTACGGCTCCCGCTTACATCATCCACGCGC 710  
QY 656 GCAATACCTTCCGCTTCCAGATGATGACGCGGCTTCCAGAACCCCAAAATTA 715  
Db 711 GCGATACGTTTGGGCGCTTAAGATATGACGAGAGGCTTGTCTAACCCCTAAGATTTG 770  
QY 716 AGGTCTCTGGGACTCGGAATGTCGAGGCTATGCGGCGGCGGCGGCGGCGGCGGCGG 775  
Db 771 AAGTGATTTGGAACTCTCGCGGCTGAGGCGGCTATGCGGCGGCGGCGGCGGCGGCGG 830  
QY 776 CTGCGGCTAAAGTTAAGAACCTACTGATGATGATGATGATGATGATGATGATGATG 835  
Db 831 GAGGATGAGGTGAGATGTTGTTACTGCGGATGTTTTCAGATCTGAAGGTGTCTGGAT 890  
QY 836 TCTTCTTCCGATCGGCGGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 895  
Db 891 TGTCTCTGCTATGCTGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 950  
QY 896 ATTACATGCTTATGCGGAAACCAACCGAGGTTTCCACTCACAACCAAGTGAAGGCTG 955  
Db 951 ATGAAGATGTTATGTTGACCAACGAGGCTACTACTAAGACGAGGCTGTTGTTGAT 1010  
QY 956 TTGCTGCTGCGGCGGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 1015  
Db 1011 TTGCTGCTGCGGATGTTCAAGACAGAGATATAGACAGGCGGCTACTCTGCGAGGACTG 1070  
QY 1016 GGTGATGCTGCTGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1075  
Db 1071 GGTGATGCTGCTGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1130  
QY 1076 AGTCTGATGA 1086  
Db 1131 AGATGATGA 1141

RESULT 10  
AAL54488  
ID AAL54488 standard; DNA; 6357 BP.  
XX AAL54488;  
XX AAL54488;  
DT 10-APR-2003 (first entry)  
XX Thioedoxin reductase variant DNA sequence #10.  
DE DE  
XX Ophthalmological; virucide; vulnerary; vasotropic; antiallergic;  
KW cofactor specificity; thioedoxin reductase; TR; non-allergenic food;

computational mutagenesis; scaffold protein; oil body; animal feed;  
digestibility; gluten; protein disulfide isomerase; PDI; enzyme;  
scleroprotein; gelled; food; nitrosative stress response; eye disease;  
cataract; oxidative stress; ischemic-reperfusion; acute lung injury; ds.  
Unidentified.  
W0200290300-A2.  
14-NOV-2002.  
06-MAY-2002; 2002WO-US014358.  
04-MAY-2001; 2001US-0289029P.  
05-APR-2002; 2002US-0370609P.  
29-APR-2002; 2002US-00370609.  
(XENC-) XENCOR.  
(SYGN) SYNGENTA PARTICIPATIONS AG.  
Briggs SP, Dalmia BK, Del Val G, Desjarlais JR, Heifetz P;  
Luginbuhl P, Muchhal U;  
WPI; 2003-111951/10.  
Altering cofactor specificity of target protein, e.g. thioedoxin  
reductase useful for reducing antigenicity of glutens in wheat, barley,  
or treating disulfide linkages present in proteins, by computational  
mutagenesis.  
Disclosure; Fig 16; 212pp; English.  
The invention relates to a novel method for altering the cofactor  
specificity of a target protein (e.g. thioedoxin reductase (TR)) by  
computational mutagenesis. This method involves inputting a set of  
coordinates for a scaffold protein comprising amino acid positions,  
applying at least one protein design cycle; and generating a set of  
candidate variant proteins with altered cofactor specificity. The novel  
method is useful for altering the cofactor specificity of TR scaffold  
proteins chosen from Escherichia coli, Bacillus subtilis, Mycobacterium  
leprae, Saccharomyces, Neurospora crassa, Arabidopsis, and human. Another  
method of the invention is useful for making oil bodies which are useful  
in the preparation of non-allergenic foods or in the preparation of  
animal feeds to improve the digestibility of the feeds. The variant TR  
protein is useful for reducing the antigenicity of glutens in wheat, rye  
or barley, to reduce alternative substrates for thioedoxin reductases,  
including a number of plant and mammalian proteins found to contain  
thioedoxin domains e.g. protein disulfide isomerase (PDI). The variant  
TR protein is useful as a redox partner in compositions used for treating  
disulfide linkages present in proteins such as enzymes, e.g. proteases,  
amylases, etc; and structural proteins such as scleroproteins.  
Compositions comprising variant TR proteins and PDI are useful for  
generating protein disulfide crosslinks yielding high molecular weight or  
gelled compositions, and thus is useful in food processing. A further  
method of the invention is useful for producing plants expressing variant  
TR protein, e.g., corn and soybean provides grains with altered storage  
protein quality as well as grains that perform qualitatively differently  
from normal grain during industrial processing or animal digestion of  
variant TR proteins in combination with thioedoxin, which can be used to  
manipulate nitrosative stress, to upregulate nitrosative stress  
responses, and thus is useful for treating eye diseases, such as  
cataracts, where it inhibits or reverse formation of cataract in eye. The  
variant TR protein in combination with thioedoxin is also useful for  
minimizing oxidative stress and ischemic-reperfusion induced in acute  
lung injury. This polynucleotide sequence represents a thioedoxin  
reductase variant DNA sequence of the invention  
Sequence 6357 BP; 1518 A; 1643 C; 1654 G; 1542 T; 0 U; 0 Other;  
Query Match 33.0%; Score 440.6; DB 7; Length 6357;  
Best Local Similarity 66.2%; Pred. No. 2.1e-90;  
Matches 657; Conservative 0; Mismatches 324; Indels 12; Gaps 1;

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Qy 108 CGCTCCGTCGGCAGCGGCATCTGCATCATCGGAGCGGTCCGCTCGCACACGGCAGC 167
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 168 CATCTAGCGGCGCGCGGAGCTCAAGCCCTGTCTCTTTCGAGGCGTGGATGCGCAACGA 227
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 228 CATCGCGCGGCGGAGCTCAAGCCCTGTCTCTTTCGAGGCGTGGATGCGCAACGA 287
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 5465 CATCGCTCCCGGTGCTCACTAAACAACACACCGAGCTGAGAAATTCGCCGGAATTC 5524
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 288 CAACGCGCATCATGCGGCGCGGAGCTCAAGCCCTGTCTCTTTCGAGGCGTGGATGCG 347
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 5525 AGRAGGTATCTCGAGTAGAGCTCACTGACAAATTCGTAACAATTCGGAGCGATTCGG 5584
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 348 CACCAACATCTCTCGAGGAGCGCTCACGCGCTGCACTTTTCGCGCTCGCATTCGAGT 407
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 5585 TACTACGATATTTACAGAGCGGTGACGAAGTGTCTTCTTCGAAACCGTTTAAGCT 5644
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 408 TAGTGCAGACTCCACACCGCTCTCGCGATGCGGTTATCGTTCGACGAGCGCGTCCG 467
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 5645 ATTACAGATTCAGAGGCAATCTCGCTGACGCTGTGATTCGCTACTGAGCTGTGGC 5704
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 468 GCGCGCTCCACTTCCCGGCTCCGAGCA-----TACTGGAACCGCGGAT 515
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 5705 TAGCGCGTGTAGCTTCGTTGATCTGCTGAGGTTCTCGAGGTTCTCGAACCGTGAAT 5764
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 516 CTCGCGCTGTGCTGTGAGCGGTGCGCCCATCTTCGTAACAGCCATCGCGCT 575
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 5765 CTCGCGATCGCTGTTCGACGAGCTGCTCGATTCGTAACAACTCTTGCGT 5824
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 576 CATAGCGGCGGAGCTCCGCTATGAGGAGTCCAAATTCCTACCAAGTACGCTCCCA 635
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 5825 GATCGGTGAGGCGATTCAGCAATGGAAGAGCAAACTTTCTTCAAAATATGATCAA 5884
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 636 CGTCTACATCATCCAGCGGCTATCTGCTGCTCCAGATCATGAGCGCGCGG 695
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 5885 AGTGTATATAATCCATCGCCCGATGCTTTTCGCTGCTTAAGATTAAGAGCGCGC 5944
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 696 GCTTGAGAACCCAAATTAAGTCTCTGCGATCTGGAAGTCTCGAGGCTATGCGCG 755
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 5945 TTTGCTTAATCTTAAGATGATGATTTGGAATCTGCTGCTGGAAGCTTATGGAGA 6004
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 756 CGCAACCGCGGCGGCTATGCTGCTGCTTAAGGTTAAGAACTACTGATGAGTCTC 815
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 6005 TCGAAGAGAGATGCTTGGAGGATTAAGAGTGAAGATGCTTACCGGTGATGTTT 6064
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 816 GGATCTTCAGGTGCTGCGCTCTTCTGCGCATCGGATGAGCGCGGACCAATTCCT 875
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 6065 TGATTAAGATTTCTGATTTGTTGCTTATTTGTTCAAGCCAGCTACCAAGTTTT 6124
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 876 GGGCGGACAGCTTGAATCGATTCAGATGTTATGTTGTAACCAAGCGAGTTCCTCA 935
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 6125 GGATGTTGTTGATTTAGTTAGTTCGATGTTTATGTTGTCAGAGGCTGTTACTACA 6184
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 936 CACAGTGTAAAGGTGTTTCTGCTGCGGATGTCGAGGACAGAGTACCTTCAGGC 995
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 6185 GACTAGCGCTTCCGAGTTTTCCCTGCGGTTGTTGTTGTTGTTGTTGTTGTTGTT 6244
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 996 CATTACTGCGCTGATCAGGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1055
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 6245 CATCACTGCTGCGGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6304
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1056 GATGTTGACAGGAGGAACTGTTGATGACT 1088
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 6305 GATTTGATCTCAGCAAGTGAAGTGAAGTGAAGT 6337
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

RESULT 11

ADD26526

ID ADD26526 standard; DNA; 6357 BP.

XX

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AC ADD26526;
XX
DT 15-JAN-2004 (first entry)
XX
DE Thalecress thioredoxin reductase RRR/S-tag/His-tag mutant DNA.
XX
KW Thioredoxin reductase; TRR; cofactor specificity;
XX computational mutagenesis; substrate specificity; PDA;
XX protein design automation; toxic protein; food allergenicity;
XX food digestibility; thalecress; ds; mutant; plant.
XX
OS Synthetic.
OS Arabidopsis thaliana.
XX
XX US2003100743-A1.
XX
XX 29-MAY-2003.
XX
XX 06-MAY-2002; 2002US-00141531.
XX
XX 04-MAY-2001; 2001US-0289029P.
XX 05-APR-2002; 2002US-0370609P.
XX 29-APR-2002; 2002US-0376682P.
XX
XX {DALM/} DALMIA B K.
XX {BRIG/} BRIGGS S P.
XX {VALG/} VAL G D.
XX {DESJ/} DESJARLAIS J R.
XX {HEIF/} HEIFETZ P.
XX {LUGI/} LUGINBUHL P.
XX {MUCH/} MUCHEAL U.
XX
XX Dalmia BK, Briggs SP, Val GD, Desjarlais JR, Heifetz P;
XX Luginbuhl P, Muchhal U;
XX WPI; 2003-801212/75.
XX
XX Altering the cofactor specificity of thioredoxin reductase, useful for
XX reducing the toxicity of toxic proteins, reducing allergenicity of food
XX and increasing the digestibility of foods, comprises computational
XX mutagenesis.
XX
XX Disclosure; Fig 16; 125pp; English.
XX
XX The invention relates to altering the cofactor specificity of thioredoxin
XX reductase (TRR) comprising computational mutagenesis. Also included are
XX altering the substrate specificity of TRR or cofactor specificity of a
XX target protein, a variant TRR protein that reduces a protein that reduces
XX a thioredoxin protein (obtained from an organism selected from
XX Escherichia coli, Bacillus subtilis, Mycobacterium leprae, Saccharomyces,
XX Neurospora crassa, Arabidopsis, and human), a variant TRR protein fused
XX to a second protein (that is either a wild-type TRR protein, thioredoxin,
XX or a variant TRR protein), producing a plant with a modified TRR protein,
XX a transformed plant prepared by the method and a transformed seed of the
XX transformed plant. The cofactor specificity of the variant TRR is altered
XX such that the variant preferentially binds NADPH compared to NADH, or
XX vice versa. The protein design cycle comprises the sequence design algorithm
XX (PDA (RTM)). This design cycle comprises the sequence design algorithm,
XX or a force field calculation. The variant TRR protein is fused to the
XX second protein through a linker. The variant TRR protein has 1-3 amino
XX acid substitutions as compared to the wild-type Arabidopsis TR protein.
XX The amino acid substitutions are selected from positions A4, A5 and A6,
XX preferably from RA4W, RA5L, RA5M, RA5I, RA5F, RA5Y, RA6T, RA6H,
XX RA6Q, RA6G, and RA6N. The method is useful for reducing the toxicity of
XX toxic proteins, reducing allergenicity of food and increasing the
XX digestibility of food. The invention provides an efficient and low cost
XX method as compared to prior art. The present sequence encodes a mutant A.
XX thaliana TRR as an S-tagged/His-tagged fusion protein.
XX
XX Sequence 6357 BP; 1518 A; 1643 C; 1654 G; 1542 T; 0 U; 0 Other;
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Query Match

33.0%; Score 440.6; DB 9; Length 6357;

Best Local Similarity 66.2%; Pred. No. 2.1e-90;



QY	408	TAGTGCAGACTCCACAAACGCTCTCGCCGATGCGGTATCGTTGCCACGGAGCGCTCGC	467
Db	5645	ATTCAAGATCCCAAGCGATCTCGCTGACGCTGTGATCTCGCTACTGAGCTGTGGC	5704
QY	468	GGGGCCCTCCACATTCGCCGGTCCGATGCA-----TACTGGAACCGCGGCAT	515
Db	5705	TAAAGCGCTTAGCTTCGTTGGATCTGGTGAAGGTTCTGGAGGTTTCTGGAAACCGTGAAT	5764
QY	516	CTCGCCCTGTGCGCTCTGTGAGGGTGGCGCCGCCATCTTCGTACAAAGCCCATCGCCGT	575
Db	5765	CTCCGATGCGCTGTTGGACGGAGCTGCTCCGATATTCGGTACAAACCTCTTGGCGGT	5824
QY	576	CATAGCGCGCGCGACTCGCTATCGGAGAGTCCAAATTCCTCCAAAGTACGGCTCCCA	635
Db	5825	GATCGGTGGAGCGGATTCAGCAATGGAAAGAACAACTTCTTACAAATATGGATCCAA	5884
QY	636	CGTCTACATCCACCGCGCAATACCTTCGCTGCTCCAGATCATCGAGGCCAGGGC	695
Db	5885	AGTGTATATAATCCATCGCTACGATGCTTTAATCGCTTAGATTTGACGAGCGGC	5944
QY	696	GCTTGAGAACCCCAAAATTAAAGTCTCTGGGACTCGGAAGTTGTCGAGGCTATGGCGG	755
Db	5945	TTTGTCTAATCTAAGATTGATGTGATTTGGAACCTGCTGTTGTGGAAGCTTATGGAGA	6004
QY	756	CGCAAGCGCGCCCATTTGCTGGCGTAAAGTTAAGAACCTACTGAAATGGTGGTCTC	815
Db	6005	TGGAGAAAGAGATGCTCTTGGAGGATTGAAGTGAAGAAATGGGTTACCGGTGATGTTT	6064
QY	816	GGATCTTCAGGTGTCTGGCTCTTCTTGGCCATCGGGCATGAGCGCGGACCCAAATTCCT	875
Db	6065	TGATTTAAAGTTTCTGGATTGTTCTTTGCTATTGTCATGAGCCAGCTACCAAGTTTT	6124
QY	876	GGCGGACAGCTTGAACCTCGATTGAGTGTATGTGGAACCAAGCCAGGTTCCACTCA	935
Db	6125	GGATGGTGTGTGAGTTAGATTGGATGGTGTATGTGTACGAAAGCCCTGGTACTACACA	6184
QY	936	CACCAAGTGTAAAGGTTGATTTTGTGCTGGCGACGTGAGGACAAAGTACCGTCAGGC	995
Db	6185	GACTAGCGTCCCGAGTTTTCGCTGCGGTGATGTTTCAAGATAGAGTATAGGCAAGC	6244
QY	996	CATTACTCGCGTGGATCAGGTTGATGCTGCTGCATTTGACGCTGAGCACTACCTGCAGGA	1055
Db	6245	CATCACTGCTGCAGGAACCTGGGTGATGGCAGCTTTGGATGACAGCATTACTTACAAGA	6304
QY	1056	GATCGGTGCACAGGAGGGAAGTCTGATTGACT	1088
Db	6305	GATTGATCTCAGCAAGGTAGAGTGTATTGACT	6337

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, PRIOR FILING DATE: 2002-04-29
, PRIOR APPLICATION NUMBER: US 10/141,531
, PRIOR FILING DATE: 2002-05-06
, PRIOR APPLICATION NUMBER: US 60/289,029
, PRIOR FILING DATE: 2001-05-04
, NUMBER OF SEQ ID NOS: 239
, SOFTWARE: PatentIn version 3.2
, SEQ ID NO 43
, LENGTH: 6357
, TYPE: DNA
, ORGANISM: Artificial sequence
, FEATURE:
, OTHER INFORMATION: synthetic
US-10-290-072-43

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Query Match	32.6%	Score 435.8	DB 13	Length 6357
Best Local Similarity	65.9%	Pred. No. 3.2e-125		
Matches 654	Conservative 0	Mismatches 327	Indels 12	Gaps 1
QY	108	CGCTCCGCTCGGCACGCGCATCTGCATCATCGGGAGCGGTCCCGCTCGGCACACGGCAGC	167	
DB	5345	CGAAACTCAACAACAAGGCTCTGTATCTGTAGGAAGTGTGCCACGGGCAACACACGGCGC	5404	
QY	168	CATCTACGGGCGCGCGGAGCTCAAGCCCTGTCTCTTTGAGGGCTGTGATGGCAACGA	227	
DB	5405	GAITTAGCAGCTAGGCTGAATTAACCTCTCTCTTCGAAGATGGATGGCTAAACGA	5464	
QY	228	CATCGCGCGGGGGGAGCTCACACACACACGAGCTGCGAGAACTTCCCGGCTTCCC	287	
DB	5465	CATCGCTCCCGGTGGTCACTAACACACACACGAGCTGTGAGAAATTTCCCGGATTTCC	5524	
QY	288	CAACGGCATCATGGGCGCGCACTCATATGGACAACTGCGCGCGCAGTCCCTGTGGCTTTGG	347	
DB	5525	AGAAGGTATTCTCGAGTAGAGCTCACTGACAAATTCGTAAACAANTCGAGCGATTCGG	5584	
QY	348	CACCAACATCCTCTCCGAGACCGTCACGCGCTCGACTTTTCGGCTGCCCATTCGAGT	407	
DB	5585	TACTACGNTATTACAGAGACGGTGAACGAAGTCAATTTCTTCTTGGAAACGCTTTAAGCT	5644	
QY	408	TAGTGCAGACTCCACAACCGTCTCTGCGCATGCGGTTATCTGTCCACGGGAGCGGTGCG	467	
DB	5645	ATTACACAGATTCCAAAGGCCATTCTCGCTGACGCTGTGATTCTCGTACTCGAGCTGTGGC	5704	
QY	468	GCGGCGCTCCACTTCCCGGCTCCGATGCA-----TACTGGAACCGCGGCAT	515	
DB	5705	TAAAGCGCTAGCTTTCGTTGATCTGGTAAAGTCTTGGAGTTCTTGGAAACGTTGAT	5764	
QY	516	CTCGCCTGTGCGCTCTGTGACGGTGGCGCCCATCTTCGTAAACAGCCCATCGCGGT	575	
DB	5765	CTCGCATGGCTGTTTGGACGAGCTGCTCCGATATTCGTGTACAAACCTCTTGGCGT	5824	
QY	576	CATAGGCGGGCGACTCCGCTATGAGGAGTCCAAATTTCTCAACAGTACGGCTCCCA	635	
DB	5825	GATGGGTGGAGCGGATTCAGCAATGGAAGAGCAAACTTTCTTACAAATATGATCCAA	5884	
QY	636	CGTCTACATCATCACCGCGCAATACTTCGCTGCTTCCAGATCATGCAAGCCAGGCG	695	
DB	5885	AGTGTATAAATCCATCGTACGATGCTTTTAATCGCTTAAGATTAATGACAGCGCGC	5944	
QY	696	GCTTGAGAACCCCAAAATTAGTTCCTCTGGGACTCGGAAGTTGTGAGGCTATGGCG	755	
DB	5945	TTTGCTCAATCCTAAGATTGATGTGAACTTGGACTCTGCTCTTTGGAGAGCTTATGAGA	6004	
QY	756	CGCAAAACGGGCGCCCATTTGGCTGGCTGAAGGTTAAGAACCTACTGAATGTGAGGTTCT	815	
DB	6005	TGGAGAAAGAGATGTGCTTGAGGATTCGAAAGTGAAGAAATGTGGTTACCGGTGATGTTTC	6064	
QY	816	GGATCTTCAGGTGTCTGCGCTCTCTTCGCCATCGGCGATGACCGCGGACCAATTCCT	875	
DB	6065	TGATTTAAAGTTTCTGGAATTTCTTTTGCTATTGGTCAAGCCAGCTACCAAGTTTTT	6124	
QY	876	GGGCGGACAGCTTGAATTCGATTCAGATGGTTATGTGGAAACCAAGCCAGGTTCCACTCA	935	

5765	Db	CTCCGATCGGCTGTTTGCAAGCAGCTGCTCCGATATTCGTAACAAACCTCTTGCGGT	5824
576	Qy	CATAGGGGGGGGCACTCCGCTATGAGGAGTCCAAATTTCTCACCAGTAGCGGCTCCCA	635
5825	Db	GATGGGTGGAGCGGATTCAGCAATGGAAGACAACTTTCTTACAAATATGGATCCAA	5884
636	Qy	CGTCTACATCATCACCGCCGCAATACCTTCGGTCTTCCAAGATCATGCAAGGCCAGGGC	695
5885	Db	AGTGTATATATCCATCGCTACGATGCTTTTAATCCGCTTAAGATATATGACAGCGCGC	5944
696	Qy	GCTTGGAGACCCCAAAATTAGTTCCTCTGGGACTCGGAAGTTGTGCGAGGCGTATGGCG	755
5945	Db	TTTGCTCAATCCTAAGATTGATGTGGACTCGTCTGTTGTGGAAGCTTATGGA	6004
756	Qy	CGCAAAACGGGGCCCATTTGGCTGGCTGAAGGTTAAGAACCTATGAAATGTGAGGTTCT	815
6005	Db	TGGAGAAAGAGATGTGCTTGAGGANTGAAAGTGAAGAAATGTGGTTACCGGTGATGTTTC	6064
816	Qy	GGATCTTCAGGTGTCTGCGCTCTCTTCGCCATCGGCGATAGCGCGGACCAAAATCCT	875
6065	Db	TGATTTAAAGTTTCTGATTTGTTCTTTTGGTATTTGGTCTAGAGCCAGCTACCAAGTTTTT	6124
876	Qy	GGGCGGACAGCTTGAACCTCGAATTCAGATGGTTATGTGGAAACCAAGCCAGGTTCCACTCA	935

QY 756 CGCAAAACGGCCGCAATGGCTGGGTAAGGTTAAGAACCTACTGAATGTGTGAGTCTC 815  
 Db 6005 TGGAGAAAGAGATGTGCTTGGAGGATTGAAAGTGAAGATGTGGTTACCGGTGATGTTT 6064  
 QY 816 GGATCTTCAGGTGTCTGCGCTCTTCTCGCCATCGGCGATGAGCGCGGACCAAAATTCCT 875  
 Db 6065 TGAATTTAAAGTTCTGGATGTCTTCTGCTATGTGCTATGAGCAGCTACCAAGTTT 6124  
 QY 876 GGGCGGACAGCTTGAATCGATTCAGATGGTATGTGAAACCAAGCAGGTTTCACTCA 935  
 Db 6125 GGATGGTGTGTTGAGTTAGATTGCGATGGTATGTTGTCGAGAGCTTGTACTACACA 6184  
 QY 936 CACCAAGTAAAGGTTGATTTGCTGCGGCTGCGGACCTGAGCAGCAAGAGTACCGTCA 995  
 Db 6185 GACTAGCGTTCCCGAGTTTTCGCTGCGGGTATGTTTCAAGTAAAGATATAGCAGC 6244  
 QY 996 CATTAAGTCCGCTGAGTCAAGGTTGATGCTGCTGATGCAATGCAAGCTGAGCACTAC 1055  
 Db 6245 CATCACTGCTGAGGAACTGGTGTGATGGCAGCTTTGGATGAGAGCACTTACTTACA 6304  
 QY 1056 GATCGGTGACAGGAGGAAAGTCTGATGACT 1088  
 Db 6305 GATTGGATCTCAGCAAGGTAAGAGTGTGGAGT 6337

## RESULT 13

US-10-141-531-38  
 ; Sequence 38, Application US/10141531  
 ; Publication No. US20030100743A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Briggs, Steven P.  
 ; APPLICANT: Dalmia, Bipin K.  
 ; APPLICANT: del Val, Greg  
 ; APPLICANT: Desjarlais, John R.  
 ; APPLICANT: Heifetz, Peter  
 ; APPLICANT: Luginbuhl, Peter  
 ; APPLICANT: Muchhal, Umesh  
 ; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity  
 ; FILE REFERENCE: A-71457-2/RFT/RMS/RMK  
 ; CURRENT APPLICATION NUMBER: US/10/141,531  
 ; CURRENT FILING DATE: 2002-05-06  
 ; PRIOR APPLICATION NUMBER: US 60/370,609  
 ; PRIOR FILING DATE: 2002-04-05  
 ; PRIOR APPLICATION NUMBER: US 60/289,029  
 ; PRIOR FILING DATE: 2001-05-04  
 ; NUMBER OF SEQ ID NOS: 208  
 ; SOFTWARE: Patent version 3.1  
 ; SEQ ID NO 38  
 ; LENGTH: 6357  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 US-10-141-531-38

Query Match 33.0%; Score 440.6; DB 15; Length 6357;  
 Best Local Similarity 66.2%; Pred. No. 9,9e-127;  
 Matches 657; Conservative 0; Mismatches 324; Indels 12; Gaps 1;  
 QY 108 CGCTCCGCTCCGCAACGCGGATCTGCAATCATCGGAGCGGTCCGCTGCGCAACGCGCAGC 167  
 Db 5345 CGAAACTCACAACAACAGGCTCTGTATCGTAGGAGTGGCCCAAGCGGCAACACGCGGCG 5404  
 QY 168 CACTAGCGGCGCGCGGAGCTCAAGCTGTGCTCTTCGAGGCTGGATGGCCCAACGA 227  
 Db 5405 GATTAGCGAGCTAGGCTGNACTTAACTCTCTTCGAGAGTGGATGGCTAACGA 5464  
 QY 228 CATCGCGCGGCGGCGGAGCTACCAACCAACGAGCTGAGAACTTCCCGGCTTCC 287  
 Db 5465 CATCGCTCCCGGTGTCAACTAACCAACCAACGAGCTGAGAACTTCCCGGATTC 5524  
 QY 288 CAACGGATCATGGCGCCGAGCTCATGGACAACTGCGCGCGCAGTCCCTGGCTTGG 347  
 Db 5525 AGAAGGTATTCTCGAGTAGAGCTCTGACAAATTCGTAACAAATCGGAGCGATTGCG 5584

QY 348 CACCAACATCTCTCCGAGACCGTCAACCGCGCTCGACTTTTCGGCTTCCCATTCGAGT 407  
 Db 5585 TACTACGATATTACAGAGACGCTGACGAAGTCGATTTCTCTCGAAACCGTTAAGCT 5644  
 QY 408 TAGTGCAGACTCCACAAACCGTCTCGCCGATGCGGTATCGTTGCCACGGAGCGCTGCG 467  
 Db 5645 ATTACAGATTTCCAAGCCCAATCTCGCTGACGCTGTGATTTCTCGCTACTCGAGCTGGC 5704  
 QY 468 GCGGCGCTCCACTTCCCGGGTCCGATGCA-----TACTGGAAACCGCGCAT 515  
 Db 5705 TAGCGGCTTAGCTTCTGTTGATCTGGTGAAGTTCTGGAGGTTCTTGGAAACCGTGAAT 5764  
 QY 516 CTCGCGCTGTGCGCTGTGTCAGGTCGCGCCCGCCATCTTCGCTAAACAGGCCATCGCGT 575  
 Db 5765 CTCGCGATGCGCTGTTTGCAGCGAGCTGCTCGATATTCGTAACAAACCTCTTGGCT 5824  
 QY 576 CATAGGCGGCGGAGCTCCGCTATGAGGAGTCCAAATTCCTCAACAGTACGCTCCCA 635  
 Db 5825 GATCGGTGGAGGCAATTCAGCATGGAAGAGCAAACTTCTTACAAAATATGGATCAA 5884  
 QY 636 CGTCTACATCATCCACCGCCCAATACCTTCGCTGCTTCCAAAGATCATGAGCGCCAGGC 695  
 Db 5885 AGTGTATATATCATCGCGGATGCTTTTTCGCTCTAAGATTATGAGCAGCGCGC 5944  
 QY 696 GCTTGAGAACCCCAAAATTAAGTCTCTGGAATCGGAAAGTTGTCGAGGCTATGCGG 755  
 Db 5945 TTTCTTAATCTTAAGATTGATGATTTGGAATCTCGTCTGTTGTTGAGCTTATGAGA 6004  
 QY 756 CGCAACCGCGCGCCCATTTGGCTGCGCTGCTGGAATTAAGATGGAAGTGTGTTACCGTGT 815  
 Db 6005 TGGAGAAAGAGATGCTGCTGAGGATTTGAAAGTGAAGATGTTGTTACCGTGTATGTT 6064  
 QY 816 GGATCTTCAGGTGTGCGCTCTTCTCGCCATCGGCGGCTGAGCGCGGCGGCGGCGGCT 875  
 Db 6065 TGATTTAAAGTTTCTGATTTCTTTGCTATTTGCTGATGAGCCAGCTACCAAGTTT 6124  
 QY 876 GGGCGGACAGCTTGAATCTGATTCAGATGGTATGAGGTTTAAAGCTTAAATGGTGAAGTCT 935  
 Db 6125 GGATGGTGTGCTGAGTTAGATTGAGTGTGTTGTTGTCAGGAAGCTTGTACTACACA 6184  
 QY 936 CACCAAGTAAAGGTTGATTTGCTGCGGAGCTGCGGCAAGTGCAGCAAGAGTACCGTCA 995  
 Db 6185 GACTAGCGTTCCCGAGTTTTCGCTGCGGGTGTGATTTGAGGATGAAGATATAGGCAAGC 6244  
 QY 996 CATTACTGCGCTGATCAGGCTGATGCGCTGATGCAATGGAGCTGAGCACTACCTGCGAGGA 1055  
 Db 6245 CATCACTGCTGAGGAACTGGGTCGATGGCAGCTTGGATGCGAGCACTTACTTACAAGA 6304  
 QY 1056 GATCGGTGACAGGAGGAAAGTCTGATGACT 1088  
 Db 6305 GATTGGATCTCAGCAAGGTAAGAGTGTGGAGT 6337

## RESULT 14

US-10-290-072-43  
 ; Sequence 43, Application US/10290072  
 ; Publication No. US20030211511A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Briggs, Steven P.  
 ; APPLICANT: Dalmia, Bipin K.  
 ; APPLICANT: del Val, Greg  
 ; APPLICANT: Desjarlais, John R.  
 ; APPLICANT: Heifetz, Peter  
 ; APPLICANT: Luginbuhl, Peter  
 ; APPLICANT: Muchhal, Umesh  
 ; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioredoxin Reductase Activity  
 ; FILE REFERENCE: A-71457-3  
 ; CURRENT APPLICATION NUMBER: US/10/290,072  
 ; CURRENT FILING DATE: 2002-11-06  
 ; PRIOR APPLICATION NUMBER: US 60/370,609  
 ; PRIOR FILING DATE: 2002-04-05  
 ; PRIOR APPLICATION NUMBER: US 60/376,682

Db 182 TTGTCATCGTGGAGTGGACCGACGACACACACCGCGCGGATCTATGTCATCGAGCGG 241  
 Qy 188 AGCTCAAGCCTGTGCTCTTGGAGGCTGGATGGCCAAACGACATCGCCGCGCGCGGCGGCG 247  
 Db 242 AGCTTAAGCCTCTTCTCTTGGAGGATGGATGGCTAAACGACATCGCTCCGCGCGGCTCAAT 301  
 Qy 248 TCACCAACACACCGACGTCGAGAACTTCCCGCGCTTCCCAACCGGATCATGGCGCGG 307  
 Db 302 TAACTACACACCGACGTCGAGAACTTCCCGCGCTTCCCAACCGGATCATGGCGGATTT 361  
 Qy 308 ACCTCATGACAACTGCGCGCGGCGAGTCCCTCGGCTTTGGGACCAACATCTCTCCGAGA 367  
 Db 362 ATATCGTGGAGAAATTCAGAAACCAATCGGAGAGATTTGGAACTACGATCTTCCGAGAA 421  
 Qy 368 CGGTCAACCGCGCTGCACTTTTCGGCTCGCCCATTCGAGTTAGTGCAGACTCCCAACCG 427  
 Db 422 CTGTAAACAAAGTGAATTTCTCATGAAACCGTTTAAAGCTATCTACTGATTCGAGACTG 481  
 Qy 428 TCTCGCCGATCGGCTTATGTTGTCACGAGAGCGCTCGCGGCGGCGCTCCACTTCCCG 487  
 Db 482 TTCTCGCTGATTTCTGTAATCATTTCTACTGCGAGCTGTTGCTAAACGCTTACTGCTCACTG 541  
 Qy 488 GGTTCGCGATGCA-----TACTGGAACCGCGGATCTCCGCGCTCGCGCTGCTG 535  
 Db 542 GATCTGGTGAAGTAATGGTGGTTTTGGATCGTGGTATCTCCGCTGGTGGTGTGG 601  
 Qy 536 ACGTGCCTCGCCCGCTTTCGTAAACAGCCCATTCGCGCTCATAGCGCGCGGCGACTCG 595  
 Db 602 ACGAGCTGCTCCGATTTTAGGAATAAGCCCTCTTGTGGTTTATTTGGTGGTGGTGAATTCAG 661  
 Qy 596 CTATGAGAGTCCCAATTTCTCACAAGTAGTGGCTCCACGCTCTACATCATCCACGCC 655  
 Db 662 CTATGAGAGAGCGAATTTCTGACTAAGTAGTGGTCTAAGTTTATTTATTTATTTATGAGA 721  
 Qy 656 GCAATACCTTCCTGCTTCCAAAGATCATGCGAGCGCGCGGCGCTTGAGAACCCCAAAATTA 715  
 Db 722 GGGATACGTTTAAAGCGCTTAAGATTTATGACGACGAGAGCTTTTGTCTAAACCTTAAGATTG 781  
 Qy 716 AGGTCTCTGCGACTCGGAAGTTGCGAGGCTATGCGCGCGCAAAACGCGCGCCATTGG 775  
 Db 782 AAGTGAATTTGGACTCTGCGGTGGTGGAGGCTATGGTGAAGAAATGGAGCTGTTCTTG 841  
 Qy 776 CTGGCGTAAAGTTAAGAACCTTCTGAATGTTGAGTCTCGATCTTCAAGTGTCTGCGC 835  
 Db 842 GAGGATTGAAGTGAAGAACTTGTGTACTGGGGATGTTTTCAGATCTGAAGGTGTCTGGAT 901  
 Qy 836 TCTTCTCGCATCGGCATGAGCGCGGACCAAAATTCCTCGCGGACAGCTTCAACTCG 895  
 Db 902 TGTCTTTGCTATTGCTCATGAGCCAGTACGAGTTTGGATGGCGAGCTTGAAGCTTG 961  
 Qy 896 ATTCAGATGGTATGTGAACCAAGCCAGGCTTCACTCAACAGGTGTAAAGGCTAT 955  
 Db 962 ATGAAGATGGTATGTTGTGACCAAGCCAGGTACTACTAAGACGAGCGTGGTGGTGTAT 1021  
 Qy 956 TTGCTGCTGCGGAGCTGCGAGGACAGAGTACCGTCAAGGCGCATTTACTGCGCTGAGTCAG 1015  
 Db 1022 TTGCTGCTGAGATGTTTCAGACAGAAAGTATAGACGCGCTTCACTGCTGAGAACTG 1081  
 Qy 1016 GGTGCATGCTGATGACCTGAGCATCTACCTGCGAGGAGATCGGTGCAAGAGGGAA 1075  
 Db 1082 GGTGCATGCGCGCATTTGATGACAGAGCAATCTTACAGAGATTTGGATCTCAGGAGGGA 1141  
 Qy 1076 AGTCTGATTGA 1086  
 Db 1142 AAGTGTATGA 1152

RESULT 12  
 US-10-290-072-38  
 ; Sequence 38, Application US/10290072  
 ; Publication No. US2003021151A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Briggs, Steven P.

; APPLICANT: Dalmia, Bipin K.  
 ; APPLICANT: Del Val, Greg  
 ; APPLICANT: Desjarlais, John R.  
 ; APPLICANT: Heifetz, Peter  
 ; APPLICANT: Luginbuhl, Peter  
 ; APPLICANT: Muchhal, Umesh  
 ; TITLE OF INVENTION: Nucleic Acids and Proteins with Thioresdoxin Reductase Activity  
 ; FILE REFERENCE: A-71457-3  
 ; CURRENT APPLICATION NUMBER: US/10/290,072  
 ; CURRENT FILING DATE: 2002-11-06  
 ; PRIOR APPLICATION NUMBER: US 60/370,609  
 ; PRIOR FILING DATE: 2002-04-05  
 ; PRIOR APPLICATION NUMBER: US 60/376,682  
 ; PRIOR FILING DATE: 2002-04-29  
 ; PRIOR APPLICATION NUMBER: US 10/141,531  
 ; PRIOR FILING DATE: 2002-05-06  
 ; PRIOR APPLICATION NUMBER: US 60/289,029  
 ; PRIOR FILING DATE: 2001-05-04  
 ; NUMBER OF SEQ ID NOS: 239  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 38  
 ; LENGTH: 6357  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 ; US-10-290-072-38

Query Match 33.0%; Score 440.6; DB 13; Length 6357;  
 Best Local Similarity 66.2%; Pred. No. 9.9e-127;  
 Matches 657; Conservative 0; Mismatches 324; Indels 12; Gaps 1;  
 Qy 108 CGCTCGCTCCGACGCGCATCTGTCATCATCGGAGCGTCCGCTCGGCACACGCGAGC 167  
 Db 5345 CGMAACTCAACAACACGAGGCTCTGTATCTAGTAAGTGGCCACGCGCACACCGCGCGC 5404  
 Qy 168 CATCTACGCGCGCGCGCGAGCTCAAGCTGTGTCTTCTGAGGCTCGATGGCCAAAGA 227  
 Db 5405 GATTACGCGAGCTAGGCTGAACCTTAAACCTCTTCTTCTGAAGGATGGATGGCTAAAGA 5464  
 Qy 228 CATCGCGCGCGCGCGAGCTCACACACACACGAGCTCGAGACTTCCCGGCTTCCC 287  
 Db 5465 CATCGCTCCGCTGGTCAACTAAACACACACGAGCTCGAGATTTCCCGGATTTCC 5524  
 Qy 288 CAACGCGCATCTGGCGCGCGACCTCATGGAACAATCGCGCGCGAGTCCCTCGCGCTTGG 347  
 Db 5525 AGAAGGATTTCTCGAGTAGAGCTCACTGACAAATTCGTTAAACAATCGGAGCGATTCCG 5584  
 Qy 348 CACCAACATCTCTCGAGACCGCTCACCGCGCTCGAGCTTTTCCGCTTCCGAGT 407  
 Db 5585 TACTACGATATTACAGAGACGCTGACGAAAGTCGATTTCTTTCGAAACCGTTTAAAGCT 5644  
 Qy 408 TAGTGCAGACTCCAAACCGCTCTCCGCGATGCGGTATCGTTGCCACGAGGAGCGCTGC 467  
 Db 5645 ATTACAGATTTCCAAAGGCGCATTTCTCGTGAAGCTGTGATTTCTGCTACTGAGGCTGGC 5704  
 Qy 468 GCGGCGCTTCCACTTCCCGGCTCCGATGCA-----TACTGGAACCGCGCAT 515  
 Db 5705 TAAGCGCTTAGCTTCTGTTGATCTGGTGAAGTTCTCGAGGTTTCTGGAACCGTGGAT 5764  
 Qy 516 CTCGCGCTGTGCGCTCTGTAGCGGTGCGCGCCCAATCTTCCGTAAACAGCCCATGCGCGT 575  
 Db 5765 CTCGCGCTGCGCTTGTGCGAGCGAGCTGCTCCGATATTCGCTAAACAACCTCTTCCGCT 5824  
 Qy 576 CATAGCGCGCGGAGCTCGCTATGAGGAGTCCCAATTTCTTCCAGTACGAGTCTCCCA 635  
 Db 5825 GATCGTGGAGCGGATTCAGCAATGGAAGAGCAACTTTCTTACAAATATGATTCNA 5884  
 Qy 636 CGTCTACATATCCACCGCGCAATACCTTCGCGCTTCCAGATCATGAGGCGCGAGGC 695  
 Db 5885 AGTGTATATATCATTCGCGCGGATGCTTTTCGTGCGTCTAAGATTTATGACGAGCGCGC 5944  
 Qy 696 GCTTGGAGAACCCCAAAATTAAGTCTCTCGGAGCTCGGAAGTTGTCGAGGCTATGCGG 755  
 Db 5945 TTGTCTAATCTTAAGATTTGATTTGAATTTGAATCTGCTCTTGTGGAAGCTTATGAGA 6004

886 CTTGAACCTCGATTGAGTGTATATGTTGAAACCAAGCCAGGTTCCACTCACACCAAGTGTGA 945  
Db CTTGAATGGAATCTGATGGGTACATTTGTTCCAAACCTGGCCACCAAGAGACTAGTGT 846  
Qy AAGGGTGTATTTGCTGCTGGGAGCTGCGAGCAAGAGTACCGTTCAGGCCATTCATGCCC 1005  
Db GATGGAGTTTGTGCTGCTGGGTGATGTTCAAGATAAAAGATATAGGCAAGCTTATACAGCT 906  
Qy GCTGATCAGGGTGCATGCTGCTGATTTGGACCTGAGCACTACCTGCGAGGAGATCGGT 1062  
Db GCTGGCACTGGGTGATGGCAGCTTGGATGCAGAACATTTACTTGCAGAGGATTTGGT 963  
RESULT 10  
US-09-938-842A-2486  
; Sequence 2486, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; TITLE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: SCRIPI300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 2486  
; LENGTH: 1152  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-2486

Query Match 34.2%; Score 457; DB 9; Length 1152;  
Best Local Similarity 67.9%; Pred. No. 3.1e-132;  
Matches 659; Conservative 0; Mismatches 300; Indels 12; Gaps 1;  
Qy 128 TCTGATCATCGGAGCGGTCCGGTGGCCACACGAGCCATCTAAGCGGCCCGCGGG 187  
Db 182 TTGTCATCTCGGAGTGGACGAGCAGACACAGCGCGCGATCTATGATCGAGAGCGG 241  
Qy 188 AGTCAAGCTGTCTTTCGAGGGCTGATGCGCAACGACATCGCGCGGGGGGCGGCG 247  
Db 242 AGCTTAAGCTCTTCTTTCGAAGGATGGATGGCTTAACGACATCGCTCCGCGCGGTCAAT 301  
Qy 248 TCACCAACCAACCGAGCTCGAACTTCCGGGCTTCCCAACGCGCATCGGCGCGG 307  
Db 302 TACTACAAACCGAGCTCGAACTTCCGGGCTTCCCTGAAGTATTCCTGATTTG 361  
Qy 308 AACTCATGACAACTCGCGCGGAGCTCCCTGGCTTTGGGCAACCAATCTCTCGAGA 367  
Db 362 ATATCGTTGAGAAATTCAGAAACAATCGAGAGATTTGGAATACGATCTTCAAGAA 421  
Qy 368 CCGTCAACCGCGGAGCTTTGGCTGCGCTGCGCATTCGAGTTAGTCAGACTCCACAACG 427  
Db 422 CTGTTAACAAGTGTATTTCTATCGAAACCGTTAAGCTATTTCATGTTTGAAGACTG 481  
Qy 428 TCTCTCCGATGCGGTATGTTTCCACGAGCGCGTTCGCGGCGCGCTCCACTTCCCGG 487  
Db 482 TTCTCGCTGATTTCTGTAATCATTTCTACTGAGCTGTGCTAAACGCTTAGCTTCACTG 541  
Qy 488 GGTCCGATGCA-----TACTGGACCGCGGATCTCCGCTGCGCTGCGCTG 535  
Db 542 GATCTGGTGAAGTAATGTTGGTGTGTTTGGAACTCGTGTATCTCCGCTGTGCTGTGG 601  
Qy 536 ACGGTGCGCGCCCATCTTCCGTAACAAGCCCATCGCGCTCATAGGCGGCGGCACTCCG 595

Db 602 ACGAGCTGCTCGAATTTTAGGAATPAGCCTTTGTGGTTATTTGGTGGTGGTGTGATTCAG 661  
Qy 596 CTATGAGGAGTCCAAATTTCTTCCCAAGTACGGCTCCCAAGCTTACATCATCCAGCGCC 655  
Db 662 CTATGAGGAGGCGAATTTCTGACTAAGTATGATCTAAGGTTTATATTTATTCATAGGA 721  
Qy 656 GCATPACCTTCCGTCTTCCAAAGTATCATGAGCCAGGGCGCTTGAGAACCCCAAAATTA 715  
Db 722 GCGATACGTTTATGGGCGTCTAAGATTATGACGAGAGAGCTTTGTCTAACCTTAAGATTG 781  
Qy 716 AGGTCTCTTGGGACTCGAAGTTGTGAGCCCTATGCGCGCGCAAAACGCGGCGCCATGCG 775  
Db 782 AAGTGAATTTGGAATCTGCGCGTGTGAGCGGTATGATGAATAATGAGACGTGTTCTTG 841  
Qy 776 CTGCGTAAAGTTTAAAGCTTACTGATGTTGAGGTTCTCGGATCTTCAAGTGTCTGGCC 835  
Db 842 GAGGATTTGAAGGTGAAGAATGTTGTTACTGCGGATGTTTCAATCTGAAGTGTCTGGAT 901  
Qy 836 TCTTCTTGGCCATCGGCGCATGAGCCGCGACCAAAATTCCTGGCGGACAGCTTGAAGCTG 895  
Db 902 TGTTCTTTGCTATTTGGTCACTAGCCAGCTACGAAGTTTGGATGGCGAGCTTGAGCTTG 961  
Qy 896 ATTCAAGTGTATGCGAAACCAAGCCAGTTCCTACACAGGCTGTAAGGGTGTAT 955  
Db 962 ATGAAGATGTTATGTTTGTGACCAAGCCAGGTACTACTAAGACGAGCGTGGTGGTGTAT 1021  
Qy 956 TTGCTGCTGGCGAGCTGCGAGCAAGAAAGTACCGTCAAGGCAATTTACTGCGCGCTGGATCAG 1015  
Db 1022 TTGCTGCTGGAGATGTTCAAGACAGAGATATAGACAGGCCATCATCTGTCAGGAACTG 1081  
Qy 1016 GGTGCATGCTGATGCGAAGCTGAGCACTTACCTGAGGAGATCGGTGCGACAGGAGGAA 1075  
Db 1082 GGTGCATGCGCGCATTTGGATGCGAGCAGCATTTACTAAGAGATTTGGATCTCAGAGGGTA 1141  
Qy 1076 AGTCTGATTGA 1086  
Db 1142 AAGTGAATTGA 1152

RESULT 11  
US-09-938-842A-2486  
; Sequence 2486, Application US/09938842A  
; Publication No. US20040009476A9  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; TITLE OF INVENTION: SAME, AND METHODS OF USE  
; FILE REFERENCE: SCRIPI300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO 2486  
; LENGTH: 1152  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-2486  
Query Match 34.2%; Score 457; DB 11; Length 1152;  
Best Local Similarity 67.9%; Pred. No. 3.1e-132;  
Matches 659; Conservative 0; Mismatches 300; Indels 12; Gaps 1;  
Qy 128 TCTGATCATCGGAGCGGTCCGGTGGCCACACGAGCCATCTAAGCGGCCCGCGGG 187

Db 64 TCTGATCATCGAAGCGGTCCTCCGCCCAACACAGCGCGTCTACCGCGCTCGAGCG 123  
Qy 188 AGCTAAGCTGTGCTCTTCGAGGGCTGATGCGCAACGACATCGCGCGGGGGGCGAGC 247  
Db 124 AGCTAAGCGGATCTCTTCGAGGGCTGATGCGCAACGACATCGCGCGGGGGGCGAGC 183  
Qy 248 TCACCAACCAACCGAGCTGAGAACTTCCCGGGCTTCCCAACGGGCGATCATCGGCGCG 307  
Db 184 TCACCAACCAACCGAGCTGAGAACTTCCCGGGCTTCCCGAGCGGCTCTCCCGGGCG 243  
Qy 308 ACCTATGAGAACTGCGCGCGAGTCCCTGCGCTTTGCGCAACATCTCTCCGAGA 367  
Db 244 AGCTCATGGAACGCTGCGGAGCGAGTCTGCTCCGCTTCGCGACCGAGATCCACACGAGA 303  
Qy 368 CCGTCAACCGCGTCTGCTTTCCGCTGCGCCATTCGAGTTAGTGCAGACTCCACAAACCG 427  
Db 304 CCGTCTCCCAAGGTCGATTTCTGAAACCGTCTCTTCAGGGTTTTCACCGATTCCCGAOCG 363  
Qy 428 TCCTCCCGGATCGGTTATCTGTCGCAACGAGGCGGTCGCGCGGCGCTCCATCTCCCG 487  
Db 364 TCGAGCGCGAATCCGTATCGTCCGCAACCGGTCGCTGCGCAAGCGGCTCTCCCTCCCG 423  
Qy 488 GGT-----CGATGATATCTGGAACCGCGCATCTCCGCTGTCGCGCTCTGTG 535  
Db 424 GCTCCGCGGACGCGCGGAGGCTACTGGAACCGTGGAACTCTCCGCTGCGCGCTGTCG 483  
Qy 536 ACCTGCGCGCGCGCATCTTCCGTAACAGCCCATCGCGCTCATAGCGCGGCGGAGCTCCG 595  
Db 484 ACGCGCGCGCGCGATCTTCCGGAACAGCGCGTGGCAGTGATCGCGCGGCGGAGACTCCG 543  
Qy 596 CTATGAGGAGTCAATTTCTCACCAGTACGCTCCGCTCCAGCTTACATCATCCACCGCC 655  
Db 544 CCATGAGGAGGACCATCTCTCACCAGTACGCTCCGAGTTCCGAGTTTACATTAATTCACG 603  
Qy 656 GCAATACCTTCCGCTCTCAAGATCATGAGGCGAGGCGCTTGAGAAACCCCAAAATTA 715  
Db 604 GGAATAGTTCAGGCTTCGAGATATGAGAGGATGATGATGATGATGATGATGATGAT 663  
Qy 716 AGTCTCTCGGACTCGGAATTTGTGAGGCTTATGCGGCTTATGCGGCGCA---AACGGGCGCCAT 772  
Db 664 AGGTGATTTGGAATTCGGTGTGTTGAGGCTTTTGGGGCGGAGATAACAAGAGGTCG 723  
Qy 773 TGCTGCGGTAAAGTTAAGAACTACTGAATGTGTAGGCTCTCGATCTTCAGTGTCTG 832  
Db 724 TTGGGGATTTGAGGTGAGAAATGCTGTGACTCAAGAGGTGTCTGAATTGAAGTTTCTG 783  
Qy 833 GCCTCTTTTCGCAATCGGCGATGAGCGCGGACCAAAATTCCTTGGCGGACAGCTTGAAC 892  
Db 784 GGTGTTTTCGCAATTTGGGCAACGAGCCCGGACCAAGTTCTTGGACGGGCGAGCTTGAAT 843  
Qy 893 TCGATTGAGTGTATGAGAAACCAAGCCAGTTCCTCACTCACCAGTGTAAAGGTTG 952  
Db 844 TGGATTCTGATGGATATATTGTGAGAGCGGGGACGACGAGACGAGTGTGAGGGAG 903  
Qy 953 TATTGCTGTCGCGACGTGCGAGCAAGAGTACCGTCAAGGCGAATTAATCTGCGCTGGAT 1012  
Db 904 TGTTTGTCTGGGATGTTTCAGGACAAAGATATAGGCAAGCTATTACTGCTGCTGGCA 963  
Qy 1013 CAGGTCATGCGCTGATTCGACGCTGAGCACTACCTCGAGGAGATCGGTGCAAGGAG 1072  
Db 964 CTGATCATGCGCTGCTTGGATGCAACATTACCTGCAAAATGTTGTTTACACAG 1023  
Qy 1073 GAAAGTCTGATTGACTATATT 1093  
Db 1024 ATAAGCTGATTGACTAGCTT 1044

RESULT 9  
US-10-424-599-13171  
; Sequence 13171, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yinhua  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 13171  
; LENGTH: 964  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_1118C.1  
US-10-424-599-13171  
  
Query Match 36.0%; Score 481.4; DB 13; Length 964;  
Best Local Similarity 69.9%; Pred. No. 6.4e-140;  
Matches 689; Conservative 0; Mismatches 276; Indels 12; Gaps 1;  
  
Qy 118 CGACGCGCATCTGCATCATCGGAGCGGTCCCGCTGCGCACACGCGAGCATCTACGCG 177  
Db 7 CGTCCGAGCTCTGCATCATCGGAGCGGCGCGGCGGCGCACACGCGCGCCATATACGCG 66  
Qy 178 GCCCGCGGAGCTCAAGCTCTGCTCTTCGAGGCTGATGCGCAACGACATCGCGCG 237  
Db 67 GCGCGCGCGAGTGAAGCGGCTCTCTTTGAAGGCTGATGCGCAACGCGTCTCC 126  
Qy 238 GCGCGGAGCTCACACCAACACCGAGCTCGAGAACTTCCCGGGCTTCCCGAAGCATC 297  
Db 127 GGTGGCGAGCTCACACCAACACCGAGCTCGAGAACTTCCCGGGATTTCCCGCGCATC 186  
Qy 298 ATGGGCGCGAGCTCATGAGCAACTGCGCGGCGGCTCTCCGCTTTCGCGCAACATC 357  
Db 187 CTCGGCACCGACTCATGACCGCTGCGCGAGCTGCGCAACGCTTTCGCGCGAGGTA 246  
Qy 358 CTCGCGAGACGCTCACCGCGCTGACATTTTCGCGCTGCGCATTCGAGTTAGTGCAGAC 417  
Db 247 GTACGAGAGCGCTCACCGCGCTGACCTCTCCACAGCTCCGTTTAGGGTTTACTCCGAC 306  
Qy 418 TCACAAACGCTCTCGCGGATGCGGTTATCTGTTCGACGCGGAGCTCTCGCGCGGCTC 477  
Db 307 TCACCAACCGCTGAGGCGGAGTCCCGTGGTGTGCGCACCGCGGCTGTGCGCAACGCTT 366  
Qy 478 CACTTCCCGGGTCC-----GATGATATCTGGAACCGCGGCTCTCCGCTGT 525  
Db 367 AATTTCGATGGCGCGGTGACACCTCTGACGGGTTCTGNAACCGCGCATATCCGCGTGC 426  
Qy 526 GCGCTCTGAGCGGTGCGCGCGGCTCTTCGCTTAACAGCCCATCGCCGCTCATAGCGGC 585  
Db 427 GCTGTGTGCGACGCGCGCGCCCAATATTCGCGCGCAACCGCTGTGTGTGATCGCGCGC 486  
Qy 586 GCGGACTCGCTATGAGGAGTCCAAATTTCTCACCAGTACGGCTCCCAACGCTCTACATC 645  
Db 487 GCGGATTCGCGGATGAGGAGGAGTACTCTCTCTCAGTTTGGCTTCAAGGTGTACATA 546  
Qy 646 ATCCACCGCGCAATACCTTCGCTTCCAGATCATCGAGGCGAGGCGCTTGAGAAC 705  
Db 547 ATTCTAGGAGGAGCAAGTTTAGGGCTTCTAAAGTCTATGAGGAGGAGTGTAGTAAT 606  
Qy 706 CCCAAATTAAGTCTCTCTGAGCTCGGAGTGTGCGGCGCTTATGCGCGCGCAACGCGC 765  
Db 607 CCCAAATTAAGTGTGTGGAATTCAGTGTGTGTTGGGCTCTGCGGATGATAGGGT 666  
Qy 766 GGCCCATTCGCTGGCGTAAAGGTTAAGAACTTCTGAATGGTGTGAGGCTCTCGGATCTTCAG 825  
Db 667 AGGATTTCTGGAGGGGTTAAGGTGAAGATGTGTGACTGGGCTCTGTCTGATTTGAAG 726  
Qy 826 GTGCTGTGGCTCTTCTTGGCATCGGCGATGAGCGCGGACCAAAATTCCTGGCGGACAG 885  
Db 727 GTTCTGAGTTGTCTTTCGAATTTGGCATGAGCCCTGCGCAAAAGTTCTTGGATGTCAT 786

Db 746 TCAAGGTGTCCGGCTCTTCTTCCCATCGCCACGAGCCGCCACCAAGTTCCTCGAGC 805  
Qy 881 GACAGCTTGAACCTGATTCAGATGTTATCTGGAACCAAGCCAGCTTCCACTCACACCA 940  
Db 806 CGGCGGTGAGCTGGATCTCGACGGCTACGTGTGACCAAGCCGGGACACACCCAGACT 865  
Qy 941 GTGTAAAGGGTGTATTTGCTGCTGGGACGTGACGACCAAGAGTACCCTCAGGCCATTA 1000  
Db 866 CCGTCCCTGCGCTGTTCCGCGCGCGGACGTGACGACCAAGAGTACCCTCAGGCCATCA 925  
Qy 1001 CTGCGCTGATCAGGGTGCATGCTGCTATTTGACCGCTGAGCACTACCTGACAGGATCG 1060  
Db 926 CCGCGCGCGGACCGCTGATGCGCGCTCTGACCGCGGACCTACCTCCAGGATCG 985  
Qy 1061 GTGCACAGGAGGAACTCTGATT 1084  
Db 986 GCTCCACGAGGCAAGTCCGACT 1009

RESULT 7  
US-10-424-599-65583  
; Sequence 65583, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 65583  
; LENGTH: 1645  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_30236C.1  
US-10-424-599-65583

Query Match 41.8%; Score 558.2; DB 13; Length 1645;  
Best Local Similarity 74.7%; Pred. No. 6.9e-164;  
Matches 733; Conservative 0; Mismatches 233; Indels 15; Gaps 2;  
Qy 128 TCTGCATCATCGGAGCGGTCCCGCTGGCGACACCGGAGCCATCTACGGCGCCCGCGG 187  
Db 176 TCTGCATCATCGGAGCGGTCCCTCCGCCCCACACAGCCCGCTCTACGCGCTCGAGCG 235  
Qy 188 AGCTCAAGCTGTGCTCTTCGAGCGCTGGATGTCACCAACGACATCGCGCGGCGGCGAGC 247  
Db 236 AGCTCAAGCTGTGCTCTTCGAGCGCTGGATGTCACCAACGACATCGCGCGGCGGCGAGC 295  
Qy 248 TCACACACACCGAGCTGAGAACTTCCCGGGCTTCCCGAAGCGGATCATGGGCGCG 307  
Db 296 TCACACACACCGAGCTGAGAACTTCCCGGGCTTCCCGAAGCGGATCATGGGCGCG 355  
Qy 308 ACCTCATGGAACATCGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 367  
Db 356 AGCTCATGGAACATCGCGCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 415  
Qy 368 CGGTCAACCGCTGCTGCTTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 427  
Db 416 CGGTCAACCGCTGCTGCTTTCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 475  
Qy 428 TCCTCGCGGATGCGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 487  
Db 476 TCAGGCGCGAATCGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 535  
Qy 488 GGT-----CCGATGCACTA CTGAAACCGCGGCACTCTCCGCTGTGCGCTGTCTGTG 535  
Db 536 GCTCCGCGATGTCGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 595

Qy 536 ACGTGTGCGCGCCCATCTTCCGTAAACAAGCCCATCCCGTTCATAGCGCGCGGACTCCG 595  
Db 596 ATGCGCGCGCGCGCATCTTCCGGNAACAAGCCCATCCCGTTCATAGCGCGCGGACTCCG 655  
Qy 596 CTATGAGAGAGTCCAAATTTCTCTCAACAAGTACCGCTCCCAAGTCTACATCATCCAGCG 655  
Db 656 CGATGAGAGAGTCCAAATTTCTCTCAACAAGTACCGCTCCCAAGTCTACATCATCCAGCG 715  
Qy 656 GCAATACCTTCCGCTGCTTCAAGATCATGAGGCGCAGGCGCTTGAAGACCCCAAAATTA 715  
Db 716 GGGATACATTCAGGCTTCCGAAGATTATGACAGACGAAGTATGGCAATAGCAAGATTA 775  
Qy 716 AGTCTCTCTGAGACTCGAAGTGTGAGGCTTATGCGGCTATGCGGCGCGCA---AAGCGGCGCCAT 772  
Db 776 AGTCTATTTGGAATTCGGTGTGCTGAGGCTTTTGGGCGCGGAGATAACAAGAGGCTGC 835  
Qy 773 TGGCTGCGGTAAAGGTTAAACAACCTACTGAATGCTGAGGCTTCTCGGATCTTCAAGTCTCTG 832  
Db 836 TTGGGGGATTTGAAGGTGAAGATGTGTGACTCGAGAGTATCTGAATTTGAAGTCTCTG 895  
Qy 833 GCCTCTTCTTCCGCTGAGCGGCGGAGCGGCGGACCAAAATTCCTGGCGCGGAGCTTGAAC 892  
Db 896 GGTGTTTTTTTCGCAATTTGGGACAGCGCGCGCAAGTCTTGGACGGGCGAGCTTGAAT 955  
Qy 893 TCGATTCAGATGTTATGCGAAACCAAGCCAGGTTCCACTCACACAGTGTAAAGGGTG 952  
Db 956 TGGATCTCTGATGATATATTGTGACGAGCCGCGGAGAGACCATGTTTGGGGAG 1015  
Qy 953 TATTGCTGCTGCGGAGCTGAGGACGAGCAAGTACCGTCAAGGCAATTAATCTGCGCTGAT 1012  
Db 1016 TGTGCTGCTGCGGAGTGTTCAGGACAAAGTATAGGCAAGCTATTAATCTGCTGCGCA 1075  
Qy 1013 CAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1072  
Db 1076 CTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1135  
Qy 1073 GAAAGTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1093  
Db 1136 ATAAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1156

RESULT 8  
US-10-425-114-29681  
; Sequence 29681, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E.  
; APPLICANT: Tabaska, Jack E.  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; FILE REFERENCE: 38-21(53313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 29681  
; LENGTH: 1284  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: UC-GMFLMINSOY117H06\_FLI  
US-10-425-114-29681  
Query Match 41.4%; Score 553.4; DB 13; Length 1284;  
Best Local Similarity 74.4%; Pred. No. 2e-162;  
Matches 730; Conservative 0; Mismatches 236; Indels 15; Gaps 2;  
Qy 128 TCTGCATCATCGGAGCGGTCCCGTGGCGACACAGGAGCCATCTACGCGCGCCCGCGG 187

GENERAL INFORMATION:  
APPLICANT: Lanahan, Michael B.  
APPLICANT: Desai, Nalini M.  
APPLICANT: Gasdaska, Pamela Y.  
TITLE OF INVENTION: GRAIN PROCESSING METHOD AND TRANSGENIC PLANTS USEFUL  
TITLE OF INVENTION: THERBIN  
FILE REFERENCE: A-31383p1  
CURRENT APPLICATION NUMBER: US/10/306,292  
PRIOR FILING DATE: 2002-11-27  
PRIOR APPLICATION NUMBER: US/09/598,747  
PRIOR FILING DATE: 2000-06-21  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 24  
LENGTH: 1021  
TYPE: DNA  
ORGANISM: Arabidopsis thaliana  
US-10-306-292-24

Query Match 42.1%; Score 562.8; DB 15; Length 1021;  
Best Local Similarity 74.2%; Pred. No. 2e-165;  
Matches 730; Conservative 0; Mismatches 242; Indels 12; Gaps 1;

QY 113 CGTCCGACGGGCATCTGCATCATCGGAGGCGTCCCGCTGGGACACGGCAGCATCT 172  
Db 26 CTCACAAACCGGCTCTGCATCTCGGCTCCGGCCGGCTCCCAACCGCGCCATCT 85  
QY 173 AGCGGCGCGCGGAGCTCAAGCTGTCTCTTCGAGGGCTGGATGGCAACGACATCG 232  
Db 86 AGCGCGCGCGCGGAGCTCAAGCTGTCTCTTCGAGGGCTGGATGGCAACGACATCG 145  
QY 233 CGCGGCGCGCGGAGCTCAAGCTGTCTCTTCGAGGGCTGGATGGCAACGACATCG 292  
Db 146 CGCGGCGCGCGGAGCTCAAGCTGTCTCTTCGAGGGCTGGATGGCAACGACATCG 205  
QY 293 GCATCTGGCGCGGAGCTCAAGCTGTCTCTTCGAGGGCTGGATGGCAACGACATCG 352  
Db 206 GCATCTGGCGCGGAGCTCAAGCTGTCTCTTCGAGGGCTGGATGGCAACGACATCG 265  
QY 353 ACATCTCTCGGAGAGCGTCAAGCTGTCTCTTCGAGGGCTGGATGGCAACGACATCG 412  
Db 266 CATCTTCACCGAGAGCGTCAAGCTGTCTCTTCGAGGGCTGGATGGCAACGACATCG 325  
QY 413 CAGACTCCACACCGTCTCGCGGAGTGGTATCGTCCAGGGAGCGTCCGCGGC 472  
Db 326 CCGACTCCAGGCGCATCTCGCGGAGTGGTATCGTCCAGGGAGCGTCCGCGGC 385  
QY 473 GCCTCCACTTCCCGCGGTC-----CGATGCATATCTGGAAACCGCGGCAATCCG 520  
Db 386 GGCTCTCTTCGCGGCTCCGCGAGTGGTATCGTCCAGGGAGCGTCCGCGGC 445  
QY 521 CTTGTGCGGTCTGTGACGCTCGCGGAGTGGTATCGTCCAGGGAGCGTCCGCGGC 580  
Db 446 CTTGTGCGGTCTGTGACGCTCGCGGAGTGGTATCGTCCAGGGAGCGTCCGCGGC 505  
QY 581 GCGGCGGAGTCTCGGTATCGGAGGAGTCCAAATTCCTCAACAGTACGGCTCCCACTCT 640  
Db 506 GTGCGGAGACAGCGGATGAGAGGAGTCCAAATTCCTCAACAGTACGGCTCCCACTCT 565  
QY 641 ACATATCCACCGCGCAATACCTTCGCTGTTCAGAGTATCGAGGCGCGGCGCTTG 700  
Db 566 ACATATCCACCGCGCAATACCTTCGCTGTTCAGAGTATCGAGGCGCGGCGCTTG 625  
QY 701 AGAACCCCAAAATTAAGTCTCTCGGAGTCCGAGTGGTTCGAGGCGCTATGCGGCGCAA 760  
Db 626 CCAACCCGAGATCGAGCTCATCTGGAACTCTCCCGTGTGGAGGCTCATCGGAGCGGCG 685  
QY 761 AGCGGCGGCGGCTGGCTGGGCTAAAGTTAAGAACTTACTGAATGTGAGTCTCGGATC 820  
Db 686 AGCGGAGTGTCTCGCGGCGCTCAAGTGAAGAACTTACTGAATGTGAGTCTCGGATC 745  
QY 821 TTCAAGTGTCTGCGCTTCTTTCGCGCATCGGCGGAGTGGCGGCGCAAAATTCCTGGCG 880

Query Match 53.0%; Score 708; DB 15; Length 1560;  
Best Local Similarity 85.0%; Pred. No. 7.4e-211;  
Matches 792; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

QY 87 AGCTATGGAGGATTCGCGCGCGCTCGCTCCCGACCGGATCTGATCATCGGAGCGG 146  
Db 402 AGCCATGGAGGATTCGCGCGCGCTCGCTCCCGACCGGATCTGATCATCGGAGCGG 461  
QY 147 TCCCGTGGGACACGCGGAGCTATACGCGGCGCGCGGAGCTCAAGCTGTCTCTT 206  
Db 462 GCGGTGGGACACGCGGAGCTATACGCGGCGCGCGGAGCTCAAGCTGTCTCTT 521  
QY 207 CGAGGCTGGATGGCGCAACGATTCGCGGCGCGGCGGAGCTCAAGCTGTCTCTT 266  
Db 522 CGAGGCTGGATGGCGCAACGATTCGCGGCGCGGCGGAGCTCAAGCTGTCTCTT 581  
QY 267 CGAGGCTGGATGGCGCAACGATTCGCGGCGCGGCGGAGCTCAAGCTGTCTCTT 326  
Db 582 CGAGGCTGGATGGCGCAACGATTCGCGGCGCGGCGGAGCTCAAGCTGTCTCTT 641  
QY 327 CGGCGAGTCTCGCTTTTGGCAACATCTCTTCGAGAGCGTCAAGCTGTCTCTT 386  
Db 642 CGGCGAGTCTCGCTTTTGGCAACATCTCTTCGAGAGCGTCAAGCTGTCTCTT 701  
QY 387 TTGCGCTGCGCATTCGAGTGTAGTGGAGTCCACAAACGCTCTCGCGCATCGGTTAT 446  
Db 702 CTCGCGCGCGCTTCGCGCTCGCTTCGAGTTCACCAACGCTCTCGCGCATCGGTTAT 761  
QY 447 CTTGCGCGCGCGCTTCGCGCTCGCTTCGAGTTCACCAACGCTCTCGCGCATCGGTTAT 506  
Db 762 CTTGCGCGCGCGCTTCGCGCTCGCTTCGAGTTCACCAACGCTCTCGCGCATCGGTTAT 821  
QY 507 CGCGGAGTCTCGCTTCGCGCTCGCTTCGAGTTCACCAACGCTCTCGCGCATCGGTTAT 566  
Db 822 CGCGGAGTCTCGCTTCGCGCTCGCTTCGAGTTCACCAACGCTCTCGCGCATCGGTTAT 881  
QY 567 CATCGCGCTCAAGCGCGCGCTTCGCGCTCGCTTCGAGTTCACCAACGCTCTCGCGCATCGGTTAT 626  
Db 882 CATCGCGCTCAAGCGCGCGCTTCGCGCTCGCTTCGAGTTCACCAACGCTCTCGCGCATCGGTTAT 941  
QY 627 CGGCTCCCGCTTACATCAACCGCGCAATCTTCGCGCTTCGAGTTCACCAACGCTCTCGCGCATCGGTTAT 686  
Db 942 CGGCTCCCGCTTACATCAACCGCGCAATCTTCGCGCTTCGAGTTCACCAACGCTCTCGCGCATCGGTTAT 1001  
QY 687 GCGGAGGCGCTTGAGAACCCCAAAATTAAGTCTCTTCGAGTTCGAGTTCGAGGCG 746  
Db 1002 GCGGAGGCGCTTGAGAACCCCAAAATTAAGTCTCTTCGAGTTCGAGTTCGAGGCG 1061  
QY 747 CTATGGGCGCGCAACCGCGCGCTTCGCGCTTCGAGTTCGAGTTCGAGGCG 806  
Db 1062 CTATGGGCGCGCAACCGCGCGCTTCGCGCTTCGAGTTCGAGTTCGAGGCG 1121  
QY 807 TGAGTCTGGATCTTCAAGTCTTCGCGCTTCGAGTTCGAGTTCGAGGCG 866  
Db 1122 TGAGTCTGGATCTTCAAGTCTTCGCGCTTCGAGTTCGAGTTCGAGGCG 1181  
QY 867 CAATTTCTCGGCGGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGGCG 926  
Db 1182 CAATTTCTCGGCGGAGTTCGAGTTCGAGTTCGAGTTCGAGTTCGAGGCG 1241  
QY 927 TTCCATCAACCGAGTAAAGTCTTCGCGCTTCGAGTTCGAGTTCGAGGCG 986  
Db 1242 TTCCATCAACCGAGTAAAGTCTTCGCGCTTCGAGTTCGAGTTCGAGGCG 1301  
QY 987 CGGTCAGGCTTATCTGCGCTGGATCAGGTT 1018  
Db 1302 CGGTCAGGCTTATCTGCGCTGGATCAGGTT 1333

RESULT 6  
US-10-306-292-24  
; Sequence 24, Application US/10306292  
; Publication No. US20030145347A1



QY 871 TTCTGGGCGGACAGCTTGAATCGATTCAGATGTTATGTGAAACCAAGCCAGGTTC 930  
DB 780 TTCTCAATGGGAGCTTGGATGCTCCATGCGGATGGATGTCGCAACCAAGCCGGCTCT 839  
QY 931 ACTCACACAGTGTAAAGGTTATTTCTGCTGGGAGCTGCAGACAGAGTACCGT 990  
DB 840 ACACATACAGTGTGAGGG-GTCTTTGCTGTGAGAGCTGCAGATGAAGTATCGT 898  
QY 991 CAGGCCATTACTGCCCTCGATCAGGGTGCATGGCTTGCAATT-GGAGCTTGACACTACT 1049  
DB 899 CAGGCCATTACTGCTGTGATCAGGTTGCATGGCTTGCTTTGGAGCGCGGACACTATCT 958  
QY 1050 GAGGAGTCTGGTGACAGAGGAGGAAGTCTGATTGA 1086  
DB 959 GCAGGAGTGGGTGCACAGGTGGGCAAGTCTGATTGA 995

RESULT 4  
US-10-091-841-23  
; Sequence 23, Application US/10091841  
; Publication No. US20030150010A1  
; GENERAL INFORMATION:  
; APPLICANT: Cho, Myeong-Je  
; APPLICANT: Del Val, Greg  
; APPLICANT: Caillaud, Maxime  
; APPLICANT: Lemaux, Peggy G.  
; APPLICANT: Buchanan, Bob B.  
; TITLE OF INVENTION: Barley Gene for Thioredoxin and  
; TITLE OF INVENTION: NADP-Thioredoxin Reductase  
; FILE REFERENCE: 2001-0701.30  
; CURRENT APPLICATION NUMBER: US/10/091,841  
; PRIOR FILING DATE: 2002-03-05  
; PRIOR APPLICATION NUMBER: 09/540,014  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: US 60/127,198  
; PRIOR FILING DATE: 1999-03-31  
; PRIOR APPLICATION NUMBER: US 60/169,162  
; PRIOR FILING DATE: 1999-12-06  
; PRIOR APPLICATION NUMBER: US 60/177,740  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: US 60/177,739  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 995  
; TYPE: DNA  
; ORGANISM: Hordeum vulgare  
US-10-091-841-23

Query Match 55.3%; Score 738.6; DB 15; Length 995;  
Best Local Similarity 85.8%; Pred. No. 1.5e-220;  
Matches 855; Conservative 0; Mismatches 139; Indels 3; Gaps 3;  
QY 91 ATGGAGGATCCCGCGCTCCGCTCCGACCGGATCTGCATCTCGGAGCGGTCC 150  
DB 1 ATGGAGGATCCCGCGCGCGCGCTCCGACCGGCTGTCATCTCGGAGCGCGCG 60  
QY 151 GCTGGCGACACCGCAGCATCTACGGCGCGCGCGGAGCTCAAGCTGTCTTCGAG 210  
DB 61 GCGCGCACACCGCGGCGCATCTAGCGCGCGCGCGGAGCTCAAGCGCTCTTCGAG 120  
QY 211 GGCTGATGCGCAACGATCTGCGCGCGCGCGGAGCTCACACACCGACCGAGCTCGAG 270  
DB 121 GGCTGATGCGCAACGATCTGCGCGCGCGCGGAGCTCACACACCGACCGAGCTCGAG 180  
QY 271 AACTTCCCGGGTTCCTCCCAACGGCATCATGGGCGCGGACCTCATGACCACTCGCGCGG 330  
DB 181 AACTTCCCGGATTCCTCCCGCGGATCATGGGCGGATCGACCTCATGACCACTCGCGCGG 240  
QY 331 CAGTCCCTGCGTTTGGGCAACATCTCTCGGAGACCGTCAACCGCGCTTCG 390  
DB 241 CAGTCCCTGCGTTTGGGCAACATCTCTCGGAGACCGTCAACCGAGTTCGATCTCTCC 300

QY 391 GCCTGCCCATTTCCAGTTAGTGCAGACTCCACAAACCGTCTCTCGCGGATGCGGTTATCGTT 450  
DB 301 GCCCGCCCTTTCCCGCTCACCTCCGACTCCACACCGTCTCTCGCGGACACCGTCTCGTCTC 360  
QY 451 GCCACGGGAGCGCTCGCGCGCGCTCCACTTTCCCGGCTCCGATGCATCTACGAAACCGC 510  
DB 361 GCCACGGGCGCGCTCGCGCGCGCTCCACTTTCTCCGGTCCGACACCTACTCGAAACCGC 420  
QY 511 GGCACTCCCGCTCGCGCTCTGTGAGCGGTGCGCGCGCTCTCTCCGTAACGACCGCTATC 570  
DB 421 GGCACTCCCGCTCGCGCTCTGTGAGCGGTGCGCGCGCTCTCTCCGTAACGACCGCTATC 480  
QY 571 GCCGTCATAGCGCGCGGCTCCGCTATGAGAGTCCAAATTTCCCTCAACAGTACGGC 630  
DB 481 GCCGTCATAGCGCGCGGCTCTCCGCTATGAGAGTCCAAATTTCCCTCAACAGTACGGC 540  
QY 631 TCCCAAGTCTATCATCTCACCGCGCGCAATCTTCCGTTTCCAAAGTATGAGGCGC 690  
DB 541 TCCCAAGTCTATCATCTCACCGCGCGCAATCTTCCGTTTCCAAAGTATGAGGCGC 600  
QY 691 AGGGCGCTTGAGAACCCCAAAATTAAGTCTCTTGGGACTCGGAGTGTGAGGCTTAT 750  
DB 601 AGGGCGCTTCTCAATCTCAAGTCCAGGTTGTCTGGGACTC-GAGGTCTGAGGCTTAC 659  
QY 751 GCGGCGCAAAACGGCGCGCTTGGCTGGCGTAAAGTAAAGAACCTTCAATGCTGAG 810  
DB 659 GCGGCTGAGCGCGCGCGCTTGGCTGGCGTAAAGTAAAGAACCTTCAATGCTGAG 719  
QY 811 GTCTCGATCTTCAAGTCTGCGCTCTTCTTCCGCTCGGAGTGTGAGGCTTAT 870  
DB 720 GTCTCGATCTTCAAGTCTGCGCTCTTCTTCCGCTCGGAGTGTGAGGCTTAT 779  
QY 871 TTCTTGGCGGACAGCTTGAATCGATTCAGATGCTTATGTGAAACCAAGCCAGGTTC 930  
DB 780 TTCTTCAATGGGAGCTTGAATCGATTCAGATGCTTATGTGAAACCAAGCCAGGTTC 839  
QY 931 ACTCACACAGTGTAAAGGTTATTTCTGCTGGGAGCTGCAGACAGAGTACCGT 990  
DB 840 ACACATACAGTGTGAGGG-GTCTTTGCTGTGAGAGCTGCAGATGAAGTATCGT 898  
QY 991 CAGGCCATTACTGCCCTCGATCAGGGTGCATGGCTTGCAATT-GGAGCTTGACACTACT 1049  
DB 899 CAGGCCATTACTGCTGTGATCAGGTTGCATGGCTTGCTTTGGAGCGCGGACACTATCT 958  
QY 1050 GCAGGAGTCTGGTGACAGGAGGGAAGTCTGATTGA 1086  
DB 959 GCAGGAGTGGGTGCACAGGTGGGCAAGTCTGATTGA 995

RESULT 5  
US-10-306-292-26  
; Sequence 26, Application US/10306292  
; Publication No. US20030145347A1  
; GENERAL INFORMATION:  
; APPLICANT: Lanahan, Michael B.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Gasdaska, Pamela Y.  
; TITLE OF INVENTION: GRAIN PROCESSING METHOD AND TRANSGENIC PLANTS USEFUL  
; TITLE OF INVENTION: THEREIN  
; FILE REFERENCE: A-31383P1  
; CURRENT APPLICATION NUMBER: US/10/306,292  
; PRIOR FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: US/09/598,747  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 26  
; LENGTH: 1560  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
US-10-306-292-26



Qy	125	GCATCTGGATC	ATCGGGAGCGGT	CCCGCTGGCG	CAACGGCAGCCAT	CTTACGGCGCCGCG	184	
Db	121	GCATCTGCATC	ATCGGGAGCGGT	CCCGCTGGCG	CAACGGCAGCCAT	CTTACGGCGCCGCG	180	
Qy	185	CGGAGCTCA	AGCCCTGTGCT	CTTCCAGAGGCT	TGGATGGCAACG	ATCCGCGCGCGGGC	244	
Db	181	CGGAGCTCA	AGCCCTGTGCT	CTTCCAGAGGCT	TGGATGGCAACG	ATCCGCGCGGGC	240	
Qy	245	AGCTCACCA	CCACCGAGT	CGAGAACT	TCCCGGCTTCC	CCCAACGGGCATCATGGGCG	304	
Db	241	AGCTCACCA	CCACCGAGT	CGAGAACT	TCCCGGCTTCC	CCCAACGGGCATCATGGGCG	300	
Qy	305	COGACCTCA	TGGACAACT	CGCGCGCG	CAGTCCCTCGCGCT	TTGGCACCACCATCTCTCCG	364	
Db	301	COGACCTCA	TGGACAACT	CGCGCGCG	CAGTCCCTCGCGCT	TTGGCACCACCATCTCTCCG	360	
Qy	365	AGAACCGT	CACCGCGCTCG	ACTTTTTCGGCGCT	CGCCATTCOGAGTT	TAGTGCAGACTCCACAA	424	
Db	361	AGAACCGT	CACCGCGCTCG	ACTTTTTCGGCGCT	CGCCATTCOGAGTT	TAGTGCAGACTCCACAA	420	
Qy	425	COGTCCTG	CGCGATGCGGTT	ATCGTTGCG	CACGGAGCGGT	TCGGCGGCGCTCCACTTCC	484	
Db	421	COGTCCTG	CGCGATGCGGTT	ATCGTTGCG	CACGGAGCGGT	TCGGCGGCGCTCCACTTCC	480	
Qy	485	COGGGTCCG	ATGTCATCTGG	AAACCGCGGC	ATCTCCGCTCTG	CGCTCTGTGACGGTGCCG	544	
Db	481	COGGGTCCG	ATGTCATCTGG	AAACCGCGGC	ATCTCCGCTCTG	CGCTCTGTGACGGTGCCG	540	
Qy	545	CCCCATCT	TCCGTAACA	AGCCCAT	CGCGTTCAT	TAGCGGGCGGCGCACTCCGCTATGAGG	604	
Db	541	CCCCATCT	TCCGTAACA	AGCCCAT	CGCGTTCAT	TAGCGGGCGGCGCACTCCGCTATGAGG	600	
Qy	605	AGTCCAA	TTTCTC	CACCAAGT	ACGGCTCC	CACGCTACATCATCCACCGCGCAATACCT	664	
Db	601	AGTCCAA	TTTCTC	CACCAAGT	ACGGCTCC	CACGCTACATCATCCACCGCGCAATACCT	660	
Qy	665	TCCGTGTCT	CCAGATCAT	CGAGCC	CAGGCGCTTG	AGAAACCCCAAAATTAAGTTCCTCT	724	
Db	661	TCCGTGTCT	CCAGATCAT	CGAGCC	CAGGCGCTTG	AGAAACCCCAAAATTAAGTTCCTCT	720	
Qy	725	GGGACTCG	GAAGTTGT	CGAGGCT	ATAGCGCG	CGCAACGGCGCCCATTCGCTGGCGTAA	784	
Db	721	GGGACTCG	GAAGTTGT	CGAGGCT	ATAGCGCG	CGCAACGGCGCCCATTCGCTGGCGTAA	780	
Qy	785	AGGTTAAG	AACTACT	GAATGGT	CAGGTCTCG	GATCTTTCAGGTCTCTGSGCTCTTCTTCG	844	
Db	781	AGGTTAAG	AACTACT	GAATGGT	CAGGTCTCG	GATCTTTCAGGTCTCTGSGCTCTTCTTCG	840	
Qy	845	CCATCGG	GCATGAC	CGCGGAC	CAAAATCT	TGCGCGGACAGCTTGAATCGATTCAGATG	904	
Db	841	CCATCGG	GCATGAC	CGCGGAC	CAAAATCT	TGCGCGGACAGCTTGAATCGATTCAGATG	900	
Qy	905	GTTATGTG	GAACCAAC	AGCCAGT	TTCATCAC	ACAGTGTAAAGGGTGATTTGCTGCTG	964	
Db	901	GTTATGTG	GAACCAAC	AGCCAGT	TTCATCAC	ACAGTGTAAAGGGTGATTTGCTGCTG	960	
Qy	965	CGCAGCT	GCAGGACA	GAAGT	ATACCGT	CAGGCAATTA	CTGCGCTGCGATACGGTGCTATGG	1024
Db	961	CGCAGCT	GCAGGACA	GAAGT	ATACCGT	CAGGCAATTA	CTGCGCTGCGATACGGTGCTATGG	1020
Qy	1025	CTGCATTT	GGACGTC	GACCTAC	CTCGCAG	GAGATCGGTGCACAGGAGGAAAGTCTGATT	1084	
Db	1021	CTGCATTT	GGACGTC	GACCTAC	CTCGCAG	GAGATCGGTGCACAGGAGGAAAGTCTGATT	1080	
Qy	1085	GACTATAT	TTTAGGT	GTAGCA	ACCGAAT	CCATCGAATAGT	TCAGTTGCGGTGCTGAAAG	1144
Db	1081	GACTATAT	TTTAGGT	GTAGCA	ACCGAAT	CCATCGAATAGT	TCAGTTGCGGTGCTGAAAG	1140
Qy	1145	COGCTCT	CTGATCG	CGCTTAT	GCATGG	TGTGATGCTACGATTCAGATACCTCGA	1204	
Db	1141	COGCTCT	CTGATCG	CGCTTAT	GCATGG	TGTGATGCTACGATTCAGATACCTCGA	1200	
Qy	1205	TGAU	TTATGCT	GTAGT	AGCAUG	CTATTCTTATCGTT	TAGGATCCAGAGTATGCTGAA	1264

[illegible]

1	1322	99.0	1325	13	US-10-425-114-3716	Sequence 3716, Ap
2	1286	96.3	1286	13	US-10-425-114-5073	Sequence 5073, Ap
3	738.6	55.3	995	15	US-10-091-841-10	Sequence 10, Appl
4	738.6	55.3	995	15	US-10-091-841-23	Sequence 23, Appl
5	708	53.0	1560	15	US-10-306-293-26	Sequence 26, Appl
6	562.8	42.1	1021	15	US-10-306-292-29	Sequence 24, Appl
7	558.2	41.8	1645	13	US-10-424-599-65583	Sequence 65583, A
8	553.4	41.4	1284	13	US-10-425-114-29581	Sequence 29581, A
9	481.4	36.0	984	13	US-10-424-559-13571	Sequence 13571, A
10	457	34.2	1152	9	US-09-938-842A-2486	Sequence 2486, Ap
11	457	34.1	1152	11	US-09-938-842A-2486	Sequence 2486, Ap
12	440.6	33.0	6357	13	US-10-390-072-38	Sequence 38, Appl
13	440.6	33.0	6357	15	US-10-391-531-38	Sequence 38, Appl
14	435.8	32.6	6357	13	US-10-140-072-43	Sequence 43, Appl

172 CAGCGGTAC-----TGATCACCAGGATGGAAGAGCGGTACGTGACC 216  
Db  
253 ACCACACGAGTCGAGACTTCGCGGCTTCCCAACGCGATCATGGGCGCGACCTC 312  
Qy  
217 ACCACGAGGAGTGGAAATTCGCGAGCGATCGAAGAGTCTACCGGTCCGCTG 276  
Db  
313 ATGACAACTCGCGCGAGTCCCTGCGTTGGCAACACATCTCTCGAGACCGTC 372  
Qy  
277 ATGAGCGCATGCACGAGCATGCGCAAAATTCGAAACCGAGATCATTTTGGACCATATC 336  
Db  
373 ACCGCGTGCATTTTCGCGCTGCCATTCGAGTTAGTGAGACTCCACACCGTCTC 432  
Qy  
337 AGCGCGTGCATTTTCCAAAACCGCGCTTCCGCTGCGTACCTGGGCTGCGTTCGAA 456  
Db  
433 GCCATGCGGTTTATCGTTGCCACGAGCGCGTTCGCGCGCGCTCCATTCGCGGGTCC 492  
Qy  
397 TGTGACGCGTATCATCGCACCGCGCTTCGCGCTTACCTGGGCTGCGTTCGAA 456  
Db  
493 GATGATATGGAACGCGCGGATCTCCGCTGCGCTGCGTCTGAGCGTCCGCGCCCATC 552  
Qy  
457 GAAGCGTTTCAAAGCGCGCGGCTTTCGCGTGGCTACCTGGGCTGCGTTCGAA 510  
Db  
553 TTCCCTAACAGCCCATCGCGCTCATAGCGCGCGCTTCGCTATGAGAGTCCAAAT 612  
Qy  
511 TATCGACACGAGAGTGGCGGTATCGCGCGCGCAACCGCAGTGGAGAGCTCTG 570  
Db  
613 TTCCTACCAAGTACGGTCCACGCTTACATCTACCGCGCGCAACCTTCCGTCGT 672  
Qy  
571 TATCTGTGGAATATCGCTCTGAGGTACACCTGATCCACCGTGGGATTCCTTCCGTCG 630  
Db  
673 TCCAGATATCATCGACGCGCGCTTGAGAA-----CCCCAAAATTAAGTCTCTC 723  
Qy  
631 GAAATAATCTCTCATCAACGCGCTGATGATAGTGGCAAGCGCAACATCGTGTGAT 690  
Db  
724 TGGGACTCGAAGTTGTGAGGCTATGCGCGCGCAACGCGCGCGCTTGGCTGGCGTA 783  
Qy  
691 ACCGATCGTACCTCGAAGAGTGCACCGCGCACAGATGGGCGTCAGCGCGCTGCGCTG 750  
Db  
784 AAGTTTAAAGACTTACTGATGAGTCTCGGATCTTCAGTGTCTGCGCTCTTCTTCTC 843  
Qy  
751 CGGATACCAA---AAACGACGACATATCGAGTCCCTGGAAGTGGCTGTTTATTTGTC 807  
Db  
844 GCATCGGCGATGAGCGCGGACCAAAATTCCTGGGCGGACAGCTTGAACGTGATCAG--- 901  
Qy  
808 GCATCGGCGCACAGCGCGGACCAACCGGCTATTTGAGGCGCGAGCTGGAGTGGAGAACGCG 867  
Db  
902 -----ATGTTATGTGAAACCAAGCCAGCTTCCACTCACACAGTGTAAAGGCTGTA 954  
Qy  
868 TACATCAAAAGTGCAGTCCGCTATCAGCAATGCAACCAAGCAAGCATCCGCGGCTG 927  
Db  
955 TTTGCTGCTGGCGAGTGCAGGACCAAGAGTACCGTACGCGCATTAATGCGCGCTGATCA 1014  
Qy  
928 TTGCGCGCGCGATGTCATGACCATATCTATCGTACGCGCATCACTTCTGCGGCGACC 987  
Db  
1015 GGTGATGCTGCTGATGACGCTGACGCTACCTGACGAGATCGGTG 1063  
Qy  
988 GGTGATGCTGCTGATGACGCTGACGCTTACCTGACGAGTGTGCTG 1036  
Db

## RESULT 15

US-09-252-991A-14492/c  
; Sequence 14492, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 14492

; LENGTH: 666

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-14492

Query Match 12.4%; Score 165.4; DB 4; Length 666;

Best Local Similarity 58.0%; Pred. No. 1.9e-31;

Matches 343; Conservative 0; Mismatches 226; Indels 22; Gaps 2;

Qy 122 CGGCGATCTGCATCATCGGAGCGGTCCTCGCTCGCACACGCGAGCAATCTAGCGGCCCC 181

Db 632 CGGCGCTCATCTCTGGGTCCGGTCCGCGCGGTATACCGCGCGGTGTAGCGCGCAC 573

Qy 182 GCGCGAGCTCAAGAGCTGTGCTCTTTCAGGGCTGATGGCGCAACGATCGCGCGCGCG 241

Db 572 GCGCGATCTCAAGCCAGTGTGTAT-----CACCGCATCCAGCAGCGG 528

Qy 242 GCGAGCTCACACACACCGAGCTCGAGAACTTCCCGGCTTCCCAACGCGCATCATGG 301

Db 527 GCGAGCTGACACACACCGAGTTCGACAACTGGCGCGGAGCTCGAAGCGCTTACCG 468

Qy 302 GCGCGGACCTCATGGAACAATGCGCGCGAGTCCCTGCGCTTGGCACCAAGATCTCT 361

Db 467 GCGCGGCGCTGATGACCGCATGCGAGCAGCAGCGCGAGCGTTTCGACACGAGATCTCT 408

Qy 362 GCGAGCGGTACCGCGCTGAGCTTTTCGCGCTGCGCAATTCGAGTTAGTGCAGACTCCA 421

Db 407 ACGACCATTCACACCGCGAGTTGCAACAGCGCGCTTCACACTGAGGCGGATAGTG 348

Qy 422 CAACCGTCTCGCGATGCGGTTATCGTTGCAACGCGAGCGTTCGCGCGCGCTTCCACT 481

Db 347 GCATTTATCTGCGATGCAATTGATCATTCGCGTCCGCGCGCAATACCTGGGCA 288

Qy 482 TCCCGGGTCCGATGATGCAATCGGAACCGCGCATCTCGCTGCGCTGTCGACGCTG 541

Db 287 TGTGTCGGAAGAAGCTTTCATGGGCAAGGCGCTTCGCTGCGCGCTGCGCGCTG 228

Qy 542 CCGCGCGCATCTTCGCTAACAGCCCAATCGCGCTGATAGGCGGCGGCGATCTCGCTATGG 601

Db 227 TT-----TCTACCGCAACCGAGTGTGCTGCGTGGTTCGCGCGCGCAATACCGCGCTG 175

Qy 602 AGGAGTCCAAATTTCTCACCAGTAAGCTCCGCTCCGAGTCTACATCATCCCGCGCAATA 661

Db 174 AGGAAGCGCTGTACTTGGCCCAACATCGCAAGGAAGTCCACCTGATCCACCGTGGGCA 115

Qy 662 CTTTCGCTGCTTCCAAAGATCATGCGAGCGCGGCGCTTGGAAACCCCAAA 712

Db 114 AGTTCGCTGCGAGAGATCTTCCAGGACAGCTGTTTCGACAGGCGCGAGA 64

Search completed: May 5, 2004, 23:29:49

Job time : 125.208 secs

COUNTRY: USA  
ZIP: 94304-1018  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows  
SOFTWARE: FastSeq for Windows Version 2.0b  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/221,017B  
FILING DATE: 23-DEC-1998  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PP1182  
FILING DATE: 31-DEC-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PP1546  
FILING DATE: 30-JAN-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PP2911  
FILING DATE: 09-APR-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/AU98/01023  
FILING DATE: 10-DEC-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Monroy, Gladys H  
REGISTRATION NUMBER: 32,430  
REFERENCE/DOCKET NUMBER: 27340-20021.00  
TELEPHONE: 650-813-5600  
TELEFAX: 650-494-0792  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 685:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1443 base pairs  
TYPE: nucleic acid  
STRANDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: UNKNOWN  
ORIGINAL SOURCE:  
ORGANISM: PORPHYROMONAS GINGIVALIS  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1...1443  
US-09-221-017B-685  
Query Match 15.1%; Score 202.4; DB 4; Length 1443;  
Best Local Similarity 53.4%; Pred. No. 2e-40;  
Matches 509; Conservative 0; Mismatches 421; Indels 24; Gaps 3;  
Qy 122 CGCGATCTGCATATCGGAGCGTCCCGCTGCGCACGAGCGCATCTACGCGGCC 181  
Db 1191 CACGCTGTCTCATCATCGGTTCCGACCTGCGCGGTATACCGGAGTATCTATGCTTCTC 1132  
Qy 182 CGCGGAGCTCAAGCTGTGCTCTTCCGAGGCTGGATGCGCAACGACATCCCGCGGCG 241  
Db 1131 GTGCCAACTCAACCCCACTCTCTACGAGG-----ATACAAACCGCGCG 1087  
Qy 242 GCGAGCTCACCACACACGAGCTGAGAACTTCCCGGCTTCCCGAACGCGATCATGG 301  
Db 1086 GTACGTAACCACTACGACGAGGTTGGAACCTTCCCGGTTATCCCGAAGGAATCAACG 1027  
Qy 302 CGCGGAGCTCATGACAACTGCGCGCGCGAGTCCCTGCTTGGCACCACCAATCTCTCT 361  
Db 1026 GTACGAACTGATGGAACCTTGGCAACAGCAACCCGCTTCCGAGCGGACATTCGTT 967  
Qy 362 CCGAGACCGTCAACCGCCCTGACATTTTCGGCTGCGCCATTCCGAGTTAGTCAGACTCCA 421  
Db 966 CGGGTATCGCTACAAAACGGATTTGACAAAGGCTCTTACAGGATCAAGATAGACGAG 907  
Qy 422 CAACCG---TCCTGCGCATCGGTTATCGTTGCGACGAGCGCTGCGCGGCGCGCTCC 478

906 AAAAGGAAATCAAGCCGATACGCTTATTATCTCCACGGGTGCCACAGC-----CAAT 853  
479 ACTTCCCGCGGTCGATGATGATGGAACCGCGGATCTCCCGCTGTGCGTCTGTGACG 538  
852 ACTTAGGCTTGGCGATGGAACCAATATAGCCGATGGTGTCTCTGTGCTACCT 793  
539 GTGCGCGCCCATCTTCCGTAACAGCCCATCGCGTATAGCGCGCGGAGTCCGCTA 598  
792 GTGATGGATTTTCTATCGCAAGAAAGTAGCCGCTAGTGGCGGAGGTGATGCTT 733  
599 TGGAGGAGTCCCAATTTCTTCCACCAAGTACGGTCCCACTCTACATCATCCACCGCGCA 658  
732 GCGAGAGGCTCTCTATCTGGGATCGTGGCTCAACACGCTGATGCTGACGCAAGA 673  
659 ATACCTTCCGCTTCCCAAGATCATCAGGCGAGGCGCTTGGAGAACCCCAAAATTAAGG 718  
672 ACTATCTCGTCTCCAAAGTAAITCAGGAGCGTGTGATGATATACGGGGAACATAACCG 613  
719 TCCTCTGGGACTCGGAAGTTGTCGAGGCTATGCGCGCGCAACCGCGGCCCATTTGGCTG 778  
612 TTCTCTCGAACAATAATACGTTGGTCTATTCCGCGAAACGCTGTGGAAGGTGCTCATC 553  
779 GCGTAAAGGTTAAGAACCTACTGAATGGTGAATCTCGGATCTTCAGGTGTCTGGCTCT 838  
552 TGGTGAACCGCAAGGAGAGCGCGACGAAGAGATGGTGGACATTGCCATCGATGTTT 493  
839 TCTTCGCATCGGCGATGAGCGCGGACCAATTCCTGGCGGCGACAGCTTGAATCGATT 898  
492 TCCTCGTATCGGTCATACGCGCAACTCGAAGATCTTCGCGGACTACCTCGACTTGGACG 433  
899 CAGATGTTATGTGAAACCAAGCCAGGTTCCACTCACACACAGTGTAAAGGTTGATTG 958  
432 AAGTGGTTATATCTTACGCGGAGGTTCTGCCCGCGCAAAAGTTCCCGGCTATTG 373  
959 CTGCTGCGGACGTCGAGGACAGAAAGTACGTCAGCGCATCTACGCGCTTGGATGAGGTT 1018  
372 CTGCGCGGACGTTGCGGACCCCACTATCGTCAGGCTATACGCGTTCGCGGATCAGGTT 313  
1019 GCATGCTGCTATGAGCGCTGAGCACTACTCTGAGGAGATGGTGCACAGGAGG 1072  
312 GCAAGCTGCTATCGAAGCAGAGCGTTATTGCGGCGAGCAGCGTCTATAAAG 259

RESULT 14  
US-09-489-039A-4925  
; Sequence 4925, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; CURRENT FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 4925  
; LENGTH: 1050  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-4925  
Query Match 13.3%; Score 178.2; DB 4; Length 1050;  
Best Local Similarity 53.6%; Pred. No. 1.6e-34;  
Matches 509; Conservative 0; Mismatches 398; Indels 42; Gaps 5;  
Qy 133 ATCATCGGAGCGTCCCGCTGCGCACGCGCAGCATCTACGCGGCCCGCGGAGCTC 192  
Db 112 ATCTTGTGTTCTGACTGCGGATACACCGCGGCTCTATGCGGACGCGCACTG 171  
Qy 193 AAGCTGTGCTCTTCGAGGCTGGATGGCAACGATCGCGCGGCGGCGAGCTCACC 252

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OTHER INFORMATION: n=a or c or g or t  
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Query Match 15.8%; Score 211.6; DB 4; Length 1230025;  
Best Local Similarity 54.8%; Pred. No. 1.2e-41;  
Matches 499; Conservative 0; Mismatches 394; Indels 21; Gaps 3;  
QY 133 ATCATCGGAGCGGTCCGCTCGCACAGCGGAGCCATCTACCGCGCCCGCGGAGCTC 192  
DB 366578 ATTATTGGTTTCAGTCCATCTGGATATACAGCGGCAATTTATGTCATCAAGAGCGCTTTG 366519  
QY 193 AACCTGTGCTCTTCGAGGCTGATGCCCAACGACATCGCGCGGCGGCGGACGCTCAC 252

DB 366518 CATCTCTTTTATTGAGGGTTTTT-----CTCTGGGACTCTGGTGGCCAGCTTATG 366465  
QY 253 ACCACCCGACGCTCGAGACTTCCCGGGCTTCCCAACGCGCATCGGGCGCCGACCTC 312  
DB 366464 ACTCAACAGAAAGTTGAGAAATTTCCAGGGTTTCTGAGGGATTTCTTGGCCAAACTT 366405  
QY 313 ATGGACAACTCGCGCGCGCATCTCCCTGCGCTTTGGCCCAACATCTCTCTCCGAGCCGCT 372  
DB 366404 ATGAATATATGAAGGAGCAGGCTGTGCGGTTTGGGACCAAGACACTAGCTCAAGATATT 366345  
QY 373 ACCGCGCTGACTTTTGGCGCTCGCATTCGAGTTAGTCAGACTCCACACCGCTCCTC 432  
DB 366344 ATTTCCGTTAGATTTTCTGTTCCGCCCTTTTATTTTGAATCAAAAGAGAAACCTTATCT 366285  
QY 433 GCCGATCGGTTTATCGTTTCCACGCGGAGCCGCTCGCGGGCGCCCTCCACTTCCCGGGTTC- 491  
DB 366284 TGTGATGCTGATCATAGCTACAGGAGCTTCTCTAAAGCTTTAGAAATTTCTTGGAGCA 366225  
QY 492 -----CGATGCTACTGGAACCGCGGATCTCCGCTGTGCGCTCTGTGAGCGGTGCCGCC 546  
DB 366224 GGAACGATGAATTTTGGCAAAAGAGTGACTCTCTTGTGCCGTTTGGATGGGGCTTCT 366165  
QY 547 CCCATCTTCCGTAACGCCCATCGCGTCAATAGCGCGCGCGGACTCCGCTATGAGGAG 606  
DB 366164 CCTATTTTAAATAAAGATCTTTATGTTGTTGGGGAGGGGATTTCTGCTTTAGAGAA 366105  
QY 607 TCCAAFTTCTCACAAGTAGTACGGTCCCACTCTACATCATCCACCGCGCAATACCTTC 666  
DB 366104 GCTCTTTACCTGACTCGTTATGGAAGCACCGTATATGTAGTTTCATGTTAGAGATAA 366045  
QY 667 CGTCTTCCAAAGATCATGCGGCGGCGGCTTTCAGAACCCCAAAATTAAGTCTCTCTGG 726  
DB 366044 CGGCTTCTAAAGCTATGGAAGCTTCGGCGCAAAACATGAATAATTTACATTTTATGG 365985  
QY 727 GACTCGGAAGTTGTGAGGCGCTATGCGGCGCAAAACCGCGGCCCATTTGGCTGGCGTAAAG 786  
DB 365984 AATAGCGAGATTGTAAATAATTTCTGGAGATAGCATGTTCTCGTTC-----CGTAGAT 365934  
QY 787 GTTAAGACCTACTGATGTTGAGGCTCTCGATCTTCAGTGTCTGCGCTCTCTCTGCC 846  
DB 365933 ATTAAGAATGTTGAGACTCAAGAATTTACAACTAGAGAGCTGCGGGGGTGTCTTTGCT 365874  
QY 847 ATCGGCGATGAGCGCGCGACCAAAATTTCTGGCGCGACAGCTTGAACCTCGATTTCAGATG 906  
DB 365873 ATAGGCCATAGCCCAATACGGATTTTCTCGGAGGACAGCTGACGTTAGATGAGTGGGC 365814  
QY 907 TATGTGAAACCAAGCCAGGTTCCACTCACACAGTGTAAAGGGTGTATTTGCTGCTGGC 966  
DB 365813 TATATTGTGACTGAGAAAGGAACGTCGAAGACTTCTGTCTCTGAGTATTTGCTGCTGGA 365754  
QY 967 GACGTGAGGCAAGAGTACCGTCAGGCCATTTACTCGCGCTGATCAGGCTGATGCT 1026  
DB 365753 GATGTTGAGATAGTACTATGCTGTCAGCGGTTACTTCTCGAGGAGGTGTTGTATAGCA 365694  
QY 1027 GCATTGAGCGCTGA 1040  
DB 365693 GCATTGAGCGCTGA 365680

RESULT 13  
US-09-221-017B-685/c  
; Sequence 685, Application US/09221017B  
; Patent No. 6444799  
; GENERAL INFORMATION:  
; APPLICANT: ROSS, Bruce C.  
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF  
; NUMBER OF SEQUENCES: 1120  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FORSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA

Db 178 GCAGCTCACCAACACCGACGTCGAGAA-TTCCCGGGCTTCCCAACGGCATCATGGG 236  
Oy 303 CGCCGACCTCATGG 316  
Db 237 CGCCGACCTCATGG 250

RESULT 12  
US-09-198-452A-1/c  
Sequence 1, Application US/09198452A  
Patent No. 6559294  
GENERAL INFORMATION:  
APPLICANT: Griffais, R.  
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments  
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention  
TITLE OF INVENTION: and treatment of infection  
FILE REFERENCE: 9710-003-999  
CURRENT APPLICATION NUMBER: US/09/198,452A  
CURRENT FILING DATE: 1998-11-24  
NUMBER OF SEQ ID NOS: 6849  
SEQ ID NO 1  
LENGTH: 1230025  
TYPE: DNA  
ORGANISM: Chlamydia pneumoniae  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)..(15000)  
OTHER INFORMATION: n=a or c or g or t  
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OTHER INFORMATION: n=a or c or g or t  
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NAME/KEY: misc feature  
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LOCATION: (255001)..(270000)  
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NAME/KEY: misc feature  
LOCATION: (585001)..(600000)  
OTHER INFORMATION: n=a or c or g or t  
NAME/KEY: misc feature





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QY 252 CACGACACCGAGCTGAGAACTTCCCGGCTTCCCAACGSCATCATGGGCGCGACCT 311
Db 4401883 GACCAACCGAGCTGGAGAACTACCCGGATTTCCGAACGSCATCACCGGTCCAGAGTT 4401942
QY 312 CATGACAACTCCCGCGCGAGTCCCTCGCTTTGGCACCAACATCTCTCCGAGACGCT 371
Db 4401943 GATGATGAGATGCGGAGACAGCGCTCGATTCGCGCGGACCTGCTATGGAAGAGCT 4402002
QY 372 CACCGCGCT-CACTTTTCGCTGCGCCATTCG--AGTTAGTGAAGATCTCACACCGT 428
Db 4402003 CGAGTCGCTATCACTTCACGCGCGCTGAATTCGCTGTCACCGCGAGACAGACCA 4402062
QY 429 CTTCCCGATGCGGTATGCTTTGTCACAGGAGCGTCGCGCGCGCTCCACTTTCCCGG 488
Db 4402063 CCGGCGCGGAGCGGTATCTGGCAATGGGCGAGCGCACGCTATCTGCAAGGTGCGCG 4402122
QY 489 GTCCGATGATGAGTGAACCGGCGATCTCCGCTGTCGCTCTGTGACGCTGCGCGCC 548
Db 4402123 CGAACGAGAAATTCGCGCGCGGCGGTGAGCTGTCGCGCCACCTGCGACG--ATT 4402176
QY 549 CATCTTCGTAAAGACCCATCGCGCTCATAGCGCGCGGCGACTCGCTATGAGAGATC 608
Db 4402177 CTTCTTCGCGATCAGACATCGCGCTCATCGCGCGGCTGACTCGGCAATGAGAGAGC 4402236
QY 609 CAATTTCTCACCAGTACGCTCCAGCTCATATCATCATCATCATCATCATCATCATCAT 668
Db 4402237 TACCTTCTGACCGCGATTCGCTGCGAGTGTGACGCTGCTGATCGCGCGAGAGTTCCG 4402296
QY 669 TGTTCCTCAAGATCATGCAAGCGCGCGCTTGAAGACCCCAAAATTAAGTCTCTCGGA 728
Db 4402297 GCTTTCCTCAAAATCATGCTGATGCGCGCGCGCGCAACAAAGACATACGTTCTCACCA 4402356
QY 729 CTCGGAAGTTCGAGGCGCTATGGGCGCGCAACGCGCGCCCATTTGGTGGCGTAAAGT 788
Db 4402357 CCACACCGTGTGCGGCTGAGCGAGGACCA-----CACTGACCGGCTTGGCGGT 4402407
QY 789 TAAGAACCTTACTGAATGTGAGGTCTCGGATCTTCAGGTGCTGGCTCTCTTCGCGCAT 848
Db 4402408 ACGGACACCAACACCGGTGCGGAACCAACCTGCGGTAAACGCTGTTCTGTCGCGAT 4402467
QY 849 CGGCGTACGCGCGGACCAAAATTCCTGGCGGAGAGCTTGGAATCGAATCAGATGTTA 908
Db 4402468 CGGCGACAGCGCGGTGCGGCTTGGTGTGCGGAGGCCATCGACGTCGACCGGACGCTA 4402527
QY 909 TGTGAAACCAAGCGAGGTCCTCACTCACACAGTGTAAAGGCTGTTATTTGCTGTCGCA 968
Db 4402528 CGTGTGTGTCAGGCGGTACCAACGACCACTCACTGCGGCGGTGTTCTGTCGCGGCA 4402587
QY 969 GTGACGACGAAGATGATACCTGAGGCGCAATTAATGCGCGCTGAGATCAGGTCGATG 1028
Db 4402588 CTTGTGTGATCGCACCTATCGCCAGGCGGTTTACCGCAGCGGCGGCTGCGCGCGCGC 4402647
QY 1029 ATTGACGCTGACACTACCTGACGAGGATCGGTGCA 1065
Db 4402648 TATCGACCGCGCGCTGGCTGCGCGGACGACGCA 4402684
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## RESULT 9

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US-09-252-991A-12680/c
; Sequence 12680, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
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; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 12680

; LENGTH: 1413

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-12680

Query Match 16.3%; Score 217.2; DB 4; Length 1413;

Best Local Similarity 54.1%; Pred. No. 4,6e-44;

Matches 528; Conservative 0; Mismatches 418; Indels 30; Gaps 3;

QY 104 CCGCGCTCCGCTCCGCGACGCGCATCTGATCATCGGAGCGGTCCGCTGCGACACGG 163

Db 1160 CGATACCTCCGCGACGCGCGAGTGATCATCTCGGTTCGCTCCGCGGTACAGCG 1101

QY 164 CAGCGATCTACCGCGCGCGCGGAGCTCAGCGTGTCTCTCGAGGCTGATGCGCA 223

Db 1100 CGGCTGTCTACCGCGCGCGCGCAACCTCAAGCGCTGCTGATCACCGGCTGCGAGGC- 1042

QY 224 ACGACATCGCGCGCGCGGCGAGCTCAACCAACACCGAGCTCGAGAACTTCCGGCT 283

Db 1041 -----GGCGCGAGTTGACCAACACCGAGTCCAGAACTGCGCGCGGCG 996

QY 284 TCCCAACCGCATCATGGCGCGGACCTCATGAGCAACTGCGCGCGCGAGTCCCTGCGCT 343

Db 995 ATCCCGCGGCTGACCGCGCGCGGACGATGAGCGGATGAGAGGACGCGCGCGCT 936

QY 344 TTGCGCAACAACTCTCTCCGAGACCGCTACCGCGCTCGACTTTTCGGCTGCGCAATTC 403

Db 935 TCGAGACCGAGATCTCTCTGACCACTTATGCGCTGAGCTGCGCGCGCAAGCGCTTCA 876

QY 404 GAGTTAGTGCACACTCCACACCGCTCTCGCGGATGCGGTATGCTGCGCGAGGCGG 463

Db 875 CCGTGTGCGGCAATGAGTACCTCACTGCGAGCACTGATCTGCGCGCGCGCTGCGCA 816

QY 464 TCGCGCGCGCTTCCACTTCTCCGCGTCCGATGCACTTGGAAACGCGCGCATCTCGGCT 523

Db 815 GCGCGCGCTTACCTGGGTTGCGCTCGAGCAGCGGTTTCAAGGCAAGGCGCTGCGGCT 756

QY 524 GTGCGCTGTGAGCGTGGCGCGCGCGCTTCTCCGCTTCAAGCGCATCGCGCTCATAGCG 583

Db 755 GCGCGACCTGCGACGCT-----TTCCTTACCGCACCGGCAAGTGGCGGTGATCGCG 702

QY 584 GCGCGACTCGCTATGAGGAGTCCAAATTTCTCAACAGTACGCTTCCACGCTTACA 643

Db 703 GCGGCAATACCGCTGTGAGAGGCGCTTACTTGGGCAACATCGCGCGGCGTACCC 642

QY 644 TCATCCACGCGCAATACCTTCCGCTTCCAGATCATGAGCGCGCGCGCTTGA 703

Db 641 TGTGCTCGTCCGCAACCTTCCGCGCGGAGAGATTTCTCCAGACAGCTGCGCGCG 582

QY 704 ACCCGAAATTAAGTCTCTTGGAGCTCGAAGTTGTGAGGCTTATGGCGCGCGCAACG 763

Db 581 GGGTGGCGGAGCAAGATAGTCTCAAGCTCAACGCGGAGTGGATGAGTGTGGCG 522

QY 764 GCGGCGCATTTGCGCTTGAAGCTTAAAGTCTTCAAGTGGTGGTCTCGGATCTTC 823

Db 521 ACAGATGGGCTCACCGCGCTGGCTGAGAGACCGGAGTGGTGGCGAGAGATCG 462

QY 824 AGGTCTGCGCTCTTCTTCCCGATCGGCGATGAGCGCGGACCAAAATTCCTGGCGGAC 883

Db 461 CGGTGATGCGATGTTCTGTCGCGCATCGGCCATCTCCCAATACCTCTGCTTTCGAGGCG 402

QY 884 AGCTTGAATCGATTCAGATGTTATGGAACCAAGCCAGTT-----CCACTC 934

Db 401 AACTGCGCTGAGAGACGCTTACTGTTGTTCAACCGGCGCGGCGGAGGCAACGCCACCG 342

QY 935 ACACAGTGTAAAGGTGTATTTCCTGTCGCGAGCTGCGAGGACAAAGTACCGTCAGG 994

Db 341 CGACCAACGTACTACCGGTGTGTTCGCGCGCGGCGAGCTGGCGGACGCTTACCGCGAG 282

QY 995 CCAATCTGCGCTGATCAGGTCGATGCTGCAATGAGGCTGAGCACTTACTGCGAGG 1054

QY 830 CTGGCTCTTCTTCCGATCGGCGATGAGCGGACCAATTCCTCGGCGACAGCTTG 889  
Db 944 ACGGCTCTTCTTACGCTGTGTGTCAGACCCCGCAGTGTCTCTCAAGGCCAGCTTG 1003  
QY 890 AACTCGATTCAGATGTTATGTGGAACCAACGACGAGTTCCACTCACACCACTGTAAAGG 949  
Db 1004 ACGTCGACGAGGATACATCATCACCAAGCCGCTACTAGCTTCACTAAGCTCGAGG 1063  
QY 950 GTGATTTGCTGCTGCGACGTCAGGACCAAGAGTACGTCAGGCCATTACTGCGCGTG 1009  
Db 1064 GTGATTTGCTGCTGCGGATGTTCAGGATAAGCGCTACCGTCAGGCTATCACCACTGCGG 1123  
QY 1010 G 1010  
Db 1124 G 1124

RESULT 7  
US-09-103-840A-2  
; Sequence 2, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; TITLE OF INVENTION: TUBERCULOSIS  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103,840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 4403765  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; FEATURE:  
; OTHER INFORMATION: CDC 1551  
; OTHER INFORMATION: "n" bases at various positions throughout the sequence  
; OTHER INFORMATION: represent a, t, c or g  
US-09-103-840A-2

Query Match 17.1%; Score 229; DB 3; Length 4403765;  
Best Local Similarity 57.0%; Pred. No. 1e-45;  
Matches 534; Conservative 0; Mismatches 370; Indels 33; Gaps 5;

QY 132 CATCATCGGAGCGGCTCGGCTGCGCACACGCGCATCATGCGGCGCGAGCT 191  
Db 4394014 CGTTATCGGCTCGGCTCGGCGGCTGACTGCGGCTCTAGCGCGCGCTGCCAGCT 4394073  
QY 192 CAAAGCTGTGCTTTTCAGGCTGGATGGCCACGACATCGCGCGCGGCGGCGAGCTCAC 251  
Db 4394074 GCGCGCGCTGTCTTCGAGCGCACGCTCTTTC-----GGCGGCGCGCTGAT 4394118  
QY 252 CACACACCGAGCTCGAGAACTTCGCGGCTTCCCAACGCGCATCATGCGGCGCGAGCT 311  
Db 4394119 GACACACCGAGCTGGAGAACTTACCGGATTTGCGACGCGATCACCGGCTCCAGATT 4394178  
QY 312 CATGACAACTGCGCGCGCGAGTTCCTGCGCTTTGGACCAACATCTCTTCGAGACCGT 371  
Db 4394179 GATGATGAGATCGCGGACAGCGGCTGCGATTCGCGCGGAGCTCGTATGGAAGCT 4394238  
QY 372 CACCGCGGT--CGACTTTTGGCTGCGCCATTCCG--AGTTAGTCAGACTCCACACCGT 428  
Db 4394239 CGAGTCGGTATCACTTACCGGCGCGTGAATCGTCTGTCACCGCGACGACAGACCA 4394298  
QY 429 CTTGCGCGGATCGGCTTATCGTTCCACGAGAGCGCTGCGCGCGCGCTCCACTTCCCGG 488  
Db 4394299 CCGGCGCGGAGCGGTGATCTGTCGAATGGCGGAGCGGACGCTATCTGAGGTGCGCG 4394358  
QY 489 GTCCGATGCACTAGGAACCGGCGATCTCCGCTGTGCGCTGTGAGCGGTGCGCGCGCC 548

Db 4394359 CGAACAGGAATFTGCTCGGCGCGGGTGAGCTGCTGCGCCACCTGCGACCG-----ATT 4394412  
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QY 609 CAATTTCTTCACCAAGTACGCTCCACAGCTCTACATCATCCACCGCGCAATACCTTCG 668  
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QY 1029 ATTGACGCTGACCACTTACCTGCGAGGAGATCGGTGCA 1065  
Db 4394884 TATCGACCGCGAGCGCTGCGCTCGCGGACGACGCA 4394920

RESULT 8  
US-09-103-840A-1  
; Sequence 1, Application US/09103840A  
; Patent No. 6294328  
; GENERAL INFORMATION:  
; APPLICANT: FLEISCHMAN, Robert D.  
; APPLICANT: WHITE, Owen R.  
; APPLICANT: FRASER, Claire M.  
; APPLICANT: VENTER, John C.  
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM  
; TITLE OF INVENTION: TUBERCULOSIS  
; FILE REFERENCE: 24366-20007.00  
; CURRENT APPLICATION NUMBER: US/09/103,840A  
; CURRENT FILING DATE: 1998-06-24  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patent in Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4411529  
; TYPE: DNA  
; ORGANISM: Mycobacterium tuberculosis  
; OTHER INFORMATION: H37Rv  
US-09-103-840A-1

Query Match 17.1%; Score 229; DB 3; Length 4411529;  
Best Local Similarity 57.0%; Pred. No. 1e-45;  
Matches 534; Conservative 0; Mismatches 370; Indels 33; Gaps 5;

QY 132 CATCATCGGAGCGGCTCGGCTGCGCACACGCGCATCATGCGGCGCGAGCT 191  
Db 4401778 CGTTATCGGCTCGGCTCGGCGGCTGACTGCGGCGCTTACGCGCGCGCTGCGCGAGCT 4401837  
QY 192 CAAAGCTGTGCTTCTGAGGCGCTGATGCGCAACACATCGCGCGGCGGCGAGCTCAC 251  
Db 4401838 GCGCGCGCTGTCTTTCGAGGCGCACTGCTTTC-----GGCGGCGCGCTGAT 4401882

Db 908 CATCACTGCTGCAGGAACCTGGGTGCATGCAGCTTTTGGATGCAGAGCATTTACTTACAGA 967

Qy 1056 GATCGGTGCACAGGAGGGGAACTCTGTATTGA 1086

Db 968 GATTGTGATCTCAGCAAGGTTAAGATGATTGA 998

## RESULT 6

RESULT 6  
 US-08-386-729A-6  
 : Sequence 6, Application US/08386729A  
 : Patent No. 5753435  
 : GENERAL INFORMATION:  
 : APPLICANT: Aharonowitz, Yair  
 : APPLICANT: Van Der Voort, Lucia H. M.  
 : APPLICANT: Cohen, Gerald  
 : APPLICANT: Bovenberg, Roelof A. L.  
 : APPLICANT: Schreiber, Rachel  
 : APPLICANT: Argaman, Anat  
 : APPLICANT: Av-Gay, Yossef  
 : APPLICANT: Nan, Helena M.  
 : APPLICANT: Kattavilder, Alfred  
 : APPLICANT: Pallissa, Harriet  
 : TITLE OF INVENTION: An oxido reductase enzyme system  
 : TITLE OF INVENTION: obtainable from P. chrysogenum, the set of genes  
 : TITLE OF INVENTION: encoding the same and the use of oxido reductase enzyme  
 : TITLE OF INVENTION: systems or genes encoding the same for increasing antibiotic  
 : TITLE OF INVENTION: production  
 : NUMBER OF SEQUENCES: 11  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Weill, Gotehal & Manges  
 : STREET: 2882 Sand Hill Road, Ste. 280  
 : CITY: Menlo Park  
 : STATE: CA  
 : COUNTRY: U.S.A.  
 : ZIP: 94025  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: 3.5" diskette  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: Patent In Release #1.0, Version #1.30  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/386,729A  
 : FILING DATE: 10-FEB-1995  
 : CLASSIFICATION: 435  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 08/274,043  
 : FILING DATE: 12-JULY-1994  
 : APPLICATION NUMBER: US 07/820,688  
 : FILING DATE: 24-MARCH-1992  
 : APPLICATION NUMBER: PCT/NL91/000101  
 : FILING DATE: 18-JUNE-1991  
 : APPLICATION NUMBER: EP 90201598.1  
 : FILING DATE: 18-JUNE-1990  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Rae-Venter, Barbara  
 : REGISTRATION NUMBER: 32,750  
 : REFERENCE/DOCKET NUMBER: GBRO-024/0205  
 : TELECOMMUNICATION INFORMATION:  
 : TELEPHONE: (415) 926-6200  
 : TELEFAX: (415) 854-3713  
 : INFORMATION FOR SEQ ID NO: 6:  
 : SEQUENCE CHARACTERISTICS:  
 : LENGTH: 1423 base pairs  
 : TYPE: nucleic acid  
 : STRANDEDNESS: double  
 : TOPOLOGY: linear  
 : MOLECULE TYPE: DNA (genomic)  
 : HYPOTHETICAL: NO  
 : ANTI-SENSE: NO  
 : ORIGINAL SOURCE:  
 : ORGANISM: Penicillium chrysogenum  
 : FEATURE:

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413 CAGACTCCCAACGCTCTCGCGATCGGGTATCGTTCCAGCGGAGCGCTCGCGCGC 472
Db      |||
326 CGACTCCCAAGGCATCTCGCGACGCGGTATCTCGCCATCGCGCGCGTGGCCAGT 385
Qy      |||
473 GCCTCCACTTCCCGGGTCTC-----CGATGCATCTGGAAACCGCGCATCTCG 520
Db      |||
386 GGCTCTCTCTCGTGGCTCGCGGAGGTGCTCGCGGCGCTCTGGAAACCGCGCATCTCG 445
Qy      |||
521 CTTGTGCGCTCTGTGAGGTGCGCGCCCATCTCTCGTACAGCCATCGCGCTATAG 580
Db      |||
446 CTTGTGCGCTCTGTGAGGTGCGCGCCCATCTCTCGTACAGCCATCGCGCTATAG 505
Qy      |||
581 GCGCGCGCGCATCTCGCTATGAGAGAGTCCAAATTCCTCAACCAAGTACGGCTCCACGCT 640
Db      |||
506 GTGGCGGAGACACGGCGATGGAGAGGCGCACTTCCTCACCAAGTACGGCTCCAGGTGT 565
Qy      |||
641 ACATATCCACCGCGCGATACCTTCGTGTGCTTCAGAGTATGAGAGGCGCGCGCTTG 700
Db      |||
566 ACATATCCACCGCGCGAGCGCTTCGCGCGCTTCAGAGTATGAGAGGCGCGCGCTTG 625
Qy      |||
701 AGAACCCCAAAATTAAGTCTCTCGGACTCGGAGTGTGCGAGGCTATGCGCGCGCAA 760
Db      |||
626 CCAACCCGAGATCGAGTCACTTGGAATCTCTCTCGTGTGAGGCTACGCGAGCGCG 685
Qy      |||
761 ACGGCGCGCGCATGCTGGCTGAAGTTAAGAACTTACATGATGTGAGGTCTCGATC 820
Db      |||
686 AGCGCGACGTCTCGCGCGCTCAAGTGAAGAACTGTGTGACCGCGAGCTGTCCGACC 745
Qy      |||
821 TTCAGTGTCTGCGCTCTCTCGCATCGGCGATGAGCGCGCGCAAAATCTCTGGCG 880
Db      |||
746 TCAAGGTGTCTGCGCTCTCTCGCATCGGCGAGCGCGCGCAAAATCTCTGGCG 805
Qy      |||
881 GACAGCTTGAACCTCGATTCAGATGTTATGTGGAACCAAGCGAGGTTCACATCACCA 940
Db      |||
806 GCGCGCTGAGCTGAGCTCGAGCGCTACGTGTGACCAAGCGCGCGCAACCCAGACT 865
Qy      |||
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US-09-540-014-26
; Sequence 26, Application US/09540014
; Patent No. 6380372
; GENERAL INFORMATION:
; APPLICANT: Cho, Myeong-Je
; APPLICANT: Del Val, Greg
; APPLICANT: Caillaud, Maxime
; APPLICANT: Lemaux, Peggy G.
; APPLICANT: Buchanan, Bob B.
; TITLE OF INVENTION: Barley Gene for Thioresdoxin and
; FILE REFERENCE: 2001-0701.30
; CURRENT APPLICATION NUMBER: US/09/540,014
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/127,198
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: US 60/169,162
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: US 60/177,740
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 60/177,739
; PRIOR FILING DATE: 2000-01-21
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; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 998
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-540-014-26
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Best Local Similarity 63.9%; Pred. No. 1.4e-84;

Matches 633; Conservative 0; Mismatches 342; Indels 16; Gaps 3;

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Db 72 GATTTACGCGAGTACGGCTGAACCTTAAACCTTCTCTTCGAGGATGATGCTTACGA 131

Qy 228 CATGCGCGCGCGCGCGAGCTTACCAACCAACGAGCTCGAGAACTTCCCGGGCTTCCC 287

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Db 249 TACTAGATATTTACAGAGACGGTGACGAACTCGATTTCTTCTGAAACCGTTTAAAGT 308

Qy 408 TAGTCGAGACTTCAACACCGTCTCGCGCGAGTTCGTTGCGTAAACAGCGCGCTCGC 467

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

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Searched: 682709 seqs, 277475446 residues

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Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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#### ALIGNMENTS

##### RESULT 1

US-09-540-014-10  
; Sequence 10, Application US/09540014  
; Patent No. 6380372  
; GENERAL INFORMATION:  
; APPLICANT: Cho, Myeong-Je  
; APPLICANT: Del Val, Greg  
; APPLICANT: Caillau, Maxime  
; APPLICANT: Lemauz, Peggy G.  
; APPLICANT: Buchanan, Bob B.  
; TITLE OF INVENTION: Barley Gene for Thioredoxin and  
; TITLE OF INVENTION: NADP-Thioredoxin Reductase  
; FILE REFERENCE: 2001-0701.30  
; CURRENT APPLICATION NUMBER: US/09/540,014  
; CURRENT FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: US 60/127,198  
; PRIOR FILING DATE: 1999-03-31  
; PRIOR APPLICATION NUMBER: US 60/169,162  
; PRIOR FILING DATE: 1999-12-06  
; PRIOR APPLICATION NUMBER: US 60/177,740  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: US 60/177,739  
; PRIOR FILING DATE: 2000-01-21  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 995  
; TYPB: DNA  
; ORGANISM: Hordeum vulgare  
US-09-540-014-10

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ACCSSION	VERSION
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AUTHORS	Walbot,V.
TITLE	Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL	University
COMMENT	Unpublished (1999) Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 606045 row: G column: 09. Location/Qualifiers 1. .588 /organism="Zea mays" /mol_type="mRNA" /cultivar="Ohio43" /db_xref="taxon:4577" /tissue_type="mixed" /dev_stage="ear length from 0.5 cm - 2.0 cm" /lab_host="XLOLR (Stratagene)" /clone_lib="606 - Ear tissue cDNA library from Schmidt lab" /note="Organ: immature ear; Vector: pBK-CMV; Site 1: EcoRI; Site 2: XhoI; Mixed ear tissue cDNA library from Schmidt lab"
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REFERENCE  
 AUTHORS  
 Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,  
 Resnick,A., Fraser,C.M., Buddiman,M.A., Bedell,J.A., Rohlfing,T.,  
 Ctek,R.W., Numbers,A., Robbins,D. and Lakey,N.  
 Consortium for Maize Genomics  
 Unpublished (2002)  
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 Contact: Cathy Whitelaw  
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TITLE  
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Universidade Estadual de Campinas	888	TGAATCTGATTCAGATGGTTATGTGGAAACCAAGCCAGGTTCCACTCACACCAAGTGTAAA	947		
Caixa Postal 6016, 13083-970, Campinas SP, Brazil	301	CGAACTTCGATTCAGATGGGATATGTTCCAAACCAACCCAGGTTCCACTCACACCAAGTGTCAA	360		
Tel: 55 19 3788 1137					
Fax: 55 19 3788 1089					
Email: parruda@unicamp.br					
Clone distribution: clone distribution information can be found					
through the Brazilian Clone Collection Center (BCCC) at					
http://www.bcccenter.fcav.unesp.br					
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FEATURES	ORIGIN				
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from polyA+ mRNA using Superscript Plasmid System Kit
(invitrogen). The double-strand cDNAs were fractionated
in a sepharose CL-2B 40cm-columns and fragments sizing
between 0.8 and 1.5 Kb were directionally cloned into the
vector. Details of each source of RNA and library
construction can be obtained at
http://sucet.lad.ic.unicamp.br/public"

ORIGIN
Query Match 45.6%; Score 609.2; DB 13; Length 678;
Best Local Similarity 95.0%; Pred. No. 1.5e-97;
Matches 629; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY 33 AACCTCTTGACACACCGCGCGCGCGGAGGCAAGCCAACTGATGAAGCAGCTAT 92
DB 10 AACCGCGCGCGCGCGCGCGCGCGGCGTGAAGCCAGCCAAACCGGTAGCAGCAT 69

QY 93 GGAGGGATCGCGCGCGCGCTCCGTCGCGCAAGCGCATCTGCATCATCGGAGCGTCCGCG 152
DB 70 GGAGGGATCGCGCGCGCGCGCTCCGTCGCGCAAGCGCGTCTGCATCATCGGAGCGCGCGCG 129

QY 153 TGGCGCACGGCAGCCATCTTACGGCGCGCGCGGAGGCTCAAGCCTGTCTCTTCAGAGG 212
DB 130 GGCGCACAGCGCAGCCATCTTACGGCGCGCGCGGAGGCTCAAGCCTGTCTCTTCAGAGG 189

QY 213 CTGGATGGCCAAACGACATCGCGCGCGCGCGGAGCTCACCACCAACCGAGCTCGAGAA 272
DB 190 CTGGATGGCCAAACGACATCGCGCGCGCGGAGGCTCACCACCAACCGAGCTCGAGAA 249

QY 273 CTTCGCGGCTTCCCAACGGGATCATGGCGCGCGGAGCTCTGAGCAACTGCGCGCGCA 332
DB 250 CTTCGCGGCTTCCCAACGGGATCATGGCGCGCGGAGCTCTGAGCAACTGCGCGCGCA 309

QY 333 GTCCCTGCGCTTTGGCACCAACATCTCTCCGAGACCGGTACCGCGCTGACCTTTTCGCG 392
DB 310 GTCCCTGCGCTTTGGCACCAACATCTCTCCGAGACCGGTACCGCGCTGACCTTTTCGCG 369

QY 393 CTGCCCATTCGAGTTAGTCAGACTCCAAACCGTCTCGCGGATCGCGTTATCGTTGC 452
DB 370 CTCCCTCTTTCGCGCTCACTGCGACTCCAAACCGTCTCGCGGATCGCGTTATCGTTGC 429

QY 453 CACGGAGCGCTCGCGCGCGCTCCACTTCCCGGGTCCGATGCACTATGGAACCGCGG 512
DB 430 CATGGGAGCGCTCGCGCGCGCTTCACTTCCCGGGTCCGATGCACTATGGAACCGCGG 489

QY 513 CATCTCGCGCTGCGCTGTGTGACGGTGGCGCGCGCGATCTTCGTAAACAGCCGATCG 572
DB 490 CATCTCGCGTGGCGCGCTGTGTGACGGTGGCGCGCGCGATCTTCGTAAACAGCCGATCG 549

QY 573 CGTCAAGCGCGCGGCGACTCCGCTATGGAGGAGTCCAAATTTCTCCACCAAGTACGGCTC 632
DB 550 TGTCATAGCGGCTGGCGACTCCGCTATGGAGGAGGCCAACTTCTCTCACCAGTATGGCTC 609

QY 633 CCAAGTCTCATCATCCACCGCGCGAATACCTTTCGCTTCCAGATCATGACGCCAG 692
DB 610 CCAAGTCTCATCATCCACCGCGCGAATACCTTTCGCTTCCAGATCATGACGCCAG 669

QY 693 GG 694
DB 670 GG 671

```

including seedlings treated with a variety of hormones

# JOURNAL COMMENT

Unpublished (2001)  
Contact: Patrick S. Schnable  
Schnable Laboratory

Iowa State University  
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA  
Tel: 515-294-0975  
Fax: 515-294-2299

Email: schnable@iastate.edu  
Individual basecall and confidence value were assigned using the

Phred software,  
(<http://depts.washington.edu/ventures/collabtr/direct/index.htm#b>  
rt). Overall sequence quality assessment and vector trimming were

conducted using the Lucy software (<http://www.tigr.org/softlab/lucy/>).  
Lucy parameters were set to ensure an overall trimmed quality of

97.5% or better without any vector fragments in the chosen  
high-quality region of each sequence. Low-quality bases between the

poly-T and the high-quality region were replaced with N's to serve

as spacers.

PCR primers

FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)

BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)

Seq primer: primer T3 (ATT AAC CCT CAC TAA AG)

## FEATURES

Location/Qualifiers  
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/organism="Zea mays"  
/mol\_type="mRNA"  
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/db\_xref="taxon:4577"  
/clone="WES272-B10"  
/tissue\_type="mixed"  
/lab\_host="DH10B"  
/clone\_lib="ISUMS-RN"

/note="Vector: pTV3PAC; Site\_1: EcoRI; Site\_2: NotI;  
Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG),  
Mixed mature tissues (17, 21, 38, 69, 77 DAG), Kernels  
(3, 5, 10, 15, 20, 25, 30, DAP), Adventitious roots (65  
DAG), Tassel (3-39 cm, 53 and 56 DAG), Immature ear  
(0.2-3.0 cm, 53, 56, 59 DAG), Husk (73 DAG), Silk,  
unpollinated first ear, ear shank, etiolated seedlings,  
callus, Cycloheximide-treated callus, Anaerobic treated  
seedlings, NAA (a-Naphthalene acetic acid)-treated  
seedlings, Kinetin-treated seedlings, ACPG  
(1-aminocyclopropane-1-carboxylic acid)-treated seedlings,  
Brassinolide-treated seedlings, ABA (Abscissic  
acid)-treated seedlings, GA (Gibberellic acid)-treated  
seedlings, JA (Jasmonic acid)-treated seedlings. ds-cDNA  
molecules were generated as follows. First-strand cDNA was  
prepared from oligo-dT selected mRNA by priming with a  
NotI oligo-dT primer (5'

AACTGGAGATTGCGCGCCGAGCAATTTTCTTTTCTTTT). The  
resulting DNA:RNA hybrid was treated with RNase H and used  
as a template for DNA PolI-catalyzed second strand  
synthesis. After the addition of EcoRI adaptors, the  
ds-cDNAs were digested with NotI and size-selected. The  
resulting molecules were directionally cloned into the  
EcoRI and NotI sites of the pTV3PAC vector. The library  
then went through one round of normalization to Cot value  
of 5 based on the methods of Marcelo Bento Soares (Genome  
Research 6: 791-806, 1996).

Research 6: 791-806, 1996).  
The resulting DNA:RNA hybrid was treated with RNase H and used  
as a template for DNA PolI-catalyzed second strand  
synthesis. After the addition of EcoRI adaptors, the  
ds-cDNAs were digested with NotI and size-selected. The  
resulting molecules were directionally cloned into the  
EcoRI and NotI sites of the pTV3PAC vector. The library  
then went through one round of normalization to Cot value  
of 5 based on the methods of Marcelo Bento Soares (Genome  
Research 6: 791-806, 1996).

## ORIGIN

Query Match 46.2%; Score 617.8; DB 12; Length 642;  
Best Local Similarity 99.7%; Pred. No. 4.5e-99;  
Matches 619; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

673 TCCAGATCATCGAGCGCGGCGTTGAGACCCCAAAATTAAGTCTCTGCGACTCG 732

642 TCCAGATCATCGAGCGCGGCGTTGAGACCCCAAAATTAAGTCTCTGCGACTCG 583

733 GAAGTTGTCGAGGCTATGCGCGCGCMAACGCGGCCCATTCGCTGGGCTAAAGGTTAAG 792

582 GAAGTTGTCGAGGCTATGCGCGCGCMAACGCGGCCCATTCGCTGGGCTAAAGGTTAAG 523

QY 793 AACCTACTGAATGTTGAGGTTCTGGATCTTTCAGGTGTTCTGCGCTCTTCTTCCCATCGGG 852  
DB 522 AACCTACTGAATGTTGAGGTTCTGGATCTTTCAGGTGTTCTGCGCTCTTCTTCCCATCGGG 463  
QY 853 CATGAGCGCGGACCAAAATTCCTGGGCGGACAGCTTGAATCCGATTCAGATGGTTATGTG 912  
DB 462 CATGAGCGCGGACCAAAATTCCTGGGCGGACAGCTTGAATCCGATTCAGATGGTTATGTG 403  
QY 913 GAAACCAAGCCAGGTTCCACTTCACACAGATGTAAAGGTTGTTATTTGCTGCTGGCGACGTG 972  
DB 402 GAAACCAAGCCAGGTTCCACTTCACACAGATGTAAAGGTTGTTATTTGCTGCTGGCGACGTG 343  
QY 973 CAGGACCAAGATACCTTCAGGCGCATTTACTGCGCTCGATCAGGTCAGGTCAGTGGCTGCAATTG 1032  
DB 342 CAGGACCAAGATACCTTCAGGCGCATTTACTGCGCTCGATCAGGTCAGGTCAGTGGCTGCAATTG 283  
QY 1033 GAGCTCTGAGCACTACCTTCAGGCGCATTTACTGCGCTCGATCAGGTCAGGTCAGTGGCTGCAATTG 1092  
DB 282 GAGCTCTGAGCACTACCTTCAGGCGCATTTACTGCGCTCGATCAGGTCAGGTCAGTGGCTGCAATTG 223  
QY 1093 TTAGGTTAGCAACAGCAATTCATGCAATAGTACGATGTCGGTGTGCGTGTGGAAGCGGCTCTC 1152  
DB 222 TTAGGTTAGCAACAGCAATTCATGCAATAGTACGATGTCGGTGTGCGTGTGGAAGCGGCTCTC 163  
QY 1153 TGATCGCGGTTTATGCCATGCTTCTTATCTTATGTTAGGATCCAGAGTATGTTGCTGCAATGATTAT 1212  
DB 162 TGATCGCGGTTTATGCCATGCTTCTTATCTTATGTTAGGATCCAGAGTATGTTGCTGCAATGATTAT 103  
QY 1213 GCTGCTTAGTAGCATGCTATTCTTATCTTATGTTAGGATCCAGAGTATGTTGCTGCAATGATTAT 1272  
DB 102 GCTGCTTAGTAGCATGCTATTCTTATCTTATGTTAGGATCCAGAGTATGTTGCTGCAATGATTAT 43  
QY 1273 TATTTACTGCACTATTTCG 1293  
DB 42 TATTTACTGCACTATTTCG 22

## RESULT 11

CA141638

LOCUS

DEFINITION

SCULRT2050E07.g RT2 Saccharum officinarum cDNA clone

5', mRNA sequence.

ACCESSION

CA141638

VERSION

CA141638.1 GI:35035827

KEYWORDS

EST.

SOURCE

Saccharum officinarum

ORGANISM

Saccharum officinarum

REFERENCE

1 (bases 1 to 678)

Authors

Vecitore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.

THE LIBRARIES THAT MADE SUCEST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

CONTACT: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parruda@unicamp.br

Clonage distribution: clone distribution information can be found

through the Brazilian Clone Collection Center (BCCC) at

<http://www.bcccenter.fcav.unesp.br>

Plate: 050 row: E column: 07

Seq primer: T7 Promoter Primer.

Location/Qualifiers

1..678

/organism="Saccharum officinarum"

/mol\_type="mRNA"

/db\_xref="taxon:4547"

/clone="SCULRT2050E07"

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Qy 154 GCGCACAGCGGAGCATTACGCGCGCGCGCGGAGCTCAAGCTGTCTTTCGAGGC 213  
Db 122 GCGCACAGCGGAGCATTACGCGCGCGCGCGGAGCTCAAGCTGTCTTTCGAGGC 181  
Qy 214 TGGATGCCACGACGATCGCGCGCGCGCGGAGCTCAAGCTGTCTTTCGAGGC 273  
Db 182 TGGATGCCACGACGATCGCGCGCGCGCGGAGCTCAAGCTGTCTTTCGAGGC 241  
Qy 274 TCCCGGGCTTCCCAAGCGGATCATGCGCGCGCGGAGCTCAAGCTGTCTTTCGAGGC 333  
Db 242 TCCCGGGCTTCCCAAGCGGATCATGCGCGCGCGGAGCTCAAGCTGTCTTTCGAGGC 301  
Qy 334 TCCCGGGCTTCCCAAGCGGATCATGCGCGCGCGGAGCTCAAGCTGTCTTTCGAGGC 393  
Db 302 TCCCGGGCTTCCCAAGCGGATCATGCGCGCGCGGAGCTCAAGCTGTCTTTCGAGGC 361  
Qy 394 TCCCGGGCTTCCCAAGCGGATCATGCGCGCGCGGAGCTCAAGCTGTCTTTCGAGGC 453  
Db 362 TCCCGGGCTTCCCAAGCGGATCATGCGCGCGCGGAGCTCAAGCTGTCTTTCGAGGC 421  
Qy 454 TCCCGGGCTTCCCAAGCGGATCATGCGCGCGCGGAGCTCAAGCTGTCTTTCGAGGC 513  
Db 422 TCCCGGGCTTCCCAAGCGGATCATGCGCGCGCGGAGCTCAAGCTGTCTTTCGAGGC 481  
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Qy 574 TCCCGGGCTTCCCAAGCGGATCATGCGCGCGCGGAGCTCAAGCTGTCTTTCGAGGC 633  
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Qy 634 TCCCGGGCTTCCCAAGCGGATCATGCGCGCGCGGAGCTCAAGCTGTCTTTCGAGGC 656  
Db 602 TCCCGGGCTTCCCAAGCGGATCATGCGCGCGCGGAGCTCAAGCTGTCTTTCGAGGC 624

RESULT 9  
CA830441  
LOCUS  
DEFINITION  
1117006H07.y1 1117 - Unigene V from Maize Genome Project Zea mays  
CDNA, mRNA sequence.  
ACCESSION  
CA830441  
VERSION  
CA830441.1 GI:26558206  
KEYWORDS  
EST.  
SOURCE  
Zea mays  
ORGANISM  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 619)  
Walbot,V.  
Maize ESTs from various cDNA libraries sequenced at Stanford  
University  
Unpublished (1999)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University  
855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Plate: 1117006 row: H column: 07.  
Location/Qualifiers  
1. 619  
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/db\_xref="dbEST:946118G10.y1"  
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/clone\_lib="1117 - Unigene V from Maize Genome Project"

/note="This library represents the unique genes found in the fifth round of EST sequencing at Stanford University for the maize genome project. Sequences are present from library 946. Contigs were assembled using ZmBAssembler and 2 representatives from each contig using ZmBAssembler the Unigene set. All singlets were also selected."

Query Match 46.3%; Score 619; DB 14; Length 619;  
Best Local Similarity 100.0%; Pred. No. 2.7e-99; Indels 0; Gaps 0;  
Matches 619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 CGCGCGCGGAGCAGCAAACTGAGTAAGCAGCTATGAGGAGGATCCGCGCGCGCTCC 113  
Db 1 CGCGCGCGGAGCAGCAAACTGAGTAAGCAGCTATGAGGAGGATCCGCGCGCGCTCC 60  
Qy 114 GCTCCGACGCGGATCTGATCATGCGGAGCGCTCCGCTGCGCACACGCGAGCCATCTA 173  
Db 61 GCTCCGACGCGGATCTGATCATGCGGAGCGCTCCGCTGCGCACACGCGAGCCATCTA 120  
Qy 174 CGCGCGCGCGGAGCAGCAAACTGAGTAAGCAGCTATGAGGAGGATCCGCGCGCGCTCC 233  
Db 121 CGCGCGCGCGGAGCAGCAAACTGAGTAAGCAGCTATGAGGAGGATCCGCGCGCGCTCC 180  
Qy 234 CGCGCGCGCGGAGCAGCAAACTGAGTAAGCAGCTATGAGGAGGATCCGCGCGCGCTCC 293  
Db 181 CGCGCGCGCGGAGCAGCAAACTGAGTAAGCAGCTATGAGGAGGATCCGCGCGCGCTCC 240  
Qy 294 CATCATGCGCGGAGCAGCAAACTGAGTAAGCAGCTATGAGGAGGATCCGCGCGCGCTCC 353  
Db 241 CATCATGCGCGGAGCAGCAAACTGAGTAAGCAGCTATGAGGAGGATCCGCGCGCGCTCC 300  
Qy 354 CATCTCTTCGAGAGCGCTCAACGCGCGGAGCAGCAAACTGAGTAAGCAGCTATGAGGAGG 413  
Db 301 CATCTCTTCGAGAGCGCTCAACGCGCGGAGCAGCAAACTGAGTAAGCAGCTATGAGGAGG 360  
Qy 414 AGACTCCACAGCGCTCCGCGGAGCAGCAAACTGAGTAAGCAGCTATGAGGAGGATCCGCGCGG 473  
Db 361 AGACTCCACAGCGCTCCGCGGAGCAGCAAACTGAGTAAGCAGCTATGAGGAGGATCCGCGCGG 420  
Qy 474 CTTCCACTTCCCGGCTCCGATGATGAGCAACGCGCGGAGCAGCAAACTGAGTAAGCAGCTATGAGGAGG 533  
Db 421 CTTCCACTTCCCGGCTCCGATGATGAGCAACGCGCGGAGCAGCAAACTGAGTAAGCAGCTATGAGGAGG 480  
Qy 534 TGAAGGTGCGCGCGGAGCAGCAAACTGAGTAAGCAGCTATGAGGAGGATCCGCGCGGAGCAGCT 593  
Db 481 TGAAGGTGCGCGCGGAGCAGCAAACTGAGTAAGCAGCTATGAGGAGGATCCGCGCGGAGCAGCT 540  
Qy 594 CGCTATGAGGAGTCCCAATTTCTCAACGAGTACGCTCCGCGGAGCAGCAAACTGAGTAAGCAGCTATGAGGAGG 653  
Db 541 CGCTATGAGGAGTCCCAATTTCTCAACGAGTACGCTCCGCGGAGCAGCAAACTGAGTAAGCAGCTATGAGGAGG 600  
Qy 654 CGCTATGAGGAGTCCCAATTTCTCAACGAGTACGCTCCGCGGAGCAGCAAACTGAGTAAGCAGCTATGAGGAGG 672  
Db 601 CGCTATGAGGAGTCCCAATTTCTCAACGAGTACGCTCCGCGGAGCAGCAAACTGAGTAAGCAGCTATGAGGAGG 619

RESULT 10  
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LOCUS  
DEFINITION  
BM351049 642 bp mRNA linear EST 15-JAN-2002  
MEST272-E10.T3 ISUM5-RN Zea mays cDNA clone MEST272-E10 3', mRNA  
sequence.  
ACCESSION  
BM351049  
VERSION  
BM351049.1 GI:18175901  
KEYWORDS  
EST.  
SOURCE  
Zea mays  
ORGANISM  
Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 642)  
Wen,T.J.; Qiu,F.; Guo,L.; Ashlock,D.A and Schnable,P.S.  
Expressed Sequence Tags from B73 Maize: various stages and tissues







686 GGAGGAGTCCAAATTTCTCCACCAAGTAGTACGGCTCCACGCTCATCATCCACGCCCGCA 745  
Db

660 TACCTTCGGTGCTTCCAAAGATCATGCGAGG 688  
Qy  
||||| ||||| ||||| ||||| |||||

746 TACCTTCGGTGCTTCAGATCATGCGAGG 774  
Db

RESULT 5					
BG842003/c					
LOCUS					
DEFINITION	BG842003	665 bp	linear	mRNA	EST 29-MAY-2001
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					sequence.

ACCESSION  
BG842003  
VERSION  
BG842003.1  
KEYWORDS  
GI:14208332  
EST.

SOURCE	ORGANISM
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zea mayas	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE	1 (bases 1 to 665)
AUTHORS	Qiu, F., Cui, F., Guo, L., Ashlock, D.A., Wen, T.J. and Schnable, P.S.
TITLE	Expressed Sequence Tags from B73 Maize Seedlings and Silks
JOURNAL	Unpublished (2001)
COMMENT	Contact: Patrick S. Schnable

**Schnable Laboratory**  
Iowa State University  
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA  
Tel: 515-294-0975  
Fax: 515-294-2208

Email: schnable@iastate.edu  
PCR Primers  
FORWARD: T7-1 (AA TAC GAC TCA CTA TAG)  
REVERSE: T7-2 (TTT GAT GAT GAT GAT GAT GAT)  
BACKWARD: T3 (ATT AAC CCT CAC TAA AG)  
T7-1 (AA TAC GAC TCA CTA TAG)  
T7-2 (TTT GAT GAT GAT GAT GAT GAT)  
T3 (ATT AAC CCT CAC TAA AG)

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/note=Vector: pT7T3PAC; Site_1: EcoRI; Site_2: NotI;
ds-cDNA molecules were generated as follows. First-strand
cDNA was prepared from oligo-dT selected mRNA by priming
with a NotI oligo-dT primer (5',

```

resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA Pol $\alpha$ -catalyzed second strand synthesis. After the addition of EcoRI adaptors, the  $\alpha$ -cDNAs were digested with NotI and size-selected. The

ORIGIN

Best Local Similarity 99.4%; Pred. No. 4.2e-106;  
Matches 660; Conservative 0; Mismatches 4; Indels 0; Gaps 0

D <sub>B</sub>	665	TCCAGGATCATGAGGCCAGGCGCTGTGGAACCCCAAAATTAAGTCTCTGGACTCG	606
Q <sub>Y</sub>	733	GAAGTTGTCGAGGCGCTATGGCGGCGCAACGGCGGCCCATTTGGCTGGGCTAAAGTTTAA	792

[illegible][illegible]

425	GAATCCAGCCAGGTTTCCACTCACACCAAGTGAAGAGGTGTAATTTCCTGCTGGCGCAAGT	366
973	CAGACAGAAGTAGTACCGTCAGGCCATTACTGCCCTGGATCAGGCTGCATGGCTGCATTG	1032
365	CAGGCACAGAAGTAGTACCGTCAGGCCATTACTGCCCTGGATCAGGCTGCATGGCTGCATTG	306

1033 GACGCTGAGCACTACCTGTCAGGGATCGGTGCACAGGAGGGAAGCTGTGATTGACTATAT 1092

Qy 1093 TTAGGTGACCAACAGCAATCCATCGAATAGTCAGTTGTGGTCTCTGAAAGCGCTC 1152  
| | | | |  
Db 245 TTAGGTGACCAACAGCAATCCATCGAATAGTCAGTTGTGGTCTCTGAAAGCGCTC 186  
| | | | |

1153 TGATCGGGTTTATGCCATGCGGTGTCATGAGCTCACGATTGAGATACCTGATGATTAT 1212  
185 TGATCGGGTTTATGCCATGCGGTGTCATGAGCTCACGATTGAGATACCTGATGATTAT 126

1213	GCCTCTAGTACATGCTATCTTATCGTTAGGATCCAGATGATGCTGAACTCTGAAC	66
125	GCCTCTAGTACATGCTATCTTATCGTTAGGATCCAGATGATGCTGAACTCTGAAC	66
1273	TATTTACTGGATACCTATCTCGTGATTAAGTGGCTTGAAGTTTTTCTTAGATATCAAAAA	1332

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Db          5 AAAA 2

RESULT 6
PROC 5557

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LOCUS	BU036557	643 bp	mRNA	linear	EST 23-AUG-2000
DEFINITION	946128A07.y1 946 - tassal primordium prepared by Schmidt lab Zea mays cDNA, mRNA sequence.				
ACCESSION	BU036557				

KEYWORDS EST.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

**REFERENCE**  
 1. (bases 1 to 643)  
 Walbot, V.  
**AUTHORS**  
 Maize ESTs from various cDNA libraries sequenced at Stanford  
**TITLE**

**JOURNAL COMMENT**  
University  
Unpublished (1999)  
Contact: Walbot V  
Department of Biological Sciences  
Stanford University

855 California Ave, Palo Alto, CA 94304, USA  
Tel: 650 723 2227  
Fax: 650 725 8221  
Email: walbot@stanford.edu  
Date: 946128 row: 3 column: 07

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FEATURES
source
Location/Qualifiers
1..643
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inflorescence development"
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resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT73PAC vector. The library was then through one round of normalization to Cot value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996)."

ORIGIN

Query Match 51.2%; Score 684; DB 12; Length 705;  
Best Local Similarity 100.0%; Pred. No. 9.3e-111; Indels 0; Gaps 0;  
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 610 AATTTCCTCAACCAAGTACGCTCCACAGCTACATCATCCACCGCGCAATACCTCCGT 669  
DB 705 AATTTCCTCAACCAAGTACGCTCCACAGCTACATCATCCACCGCGCAATACCTCCGT 646  
QY 670 GCTTCGAAGTATCATGCGGCGAGGCGCTTGAGAACCCCAAAATTAAGTCTCTCGGAC 729  
DB 645 GCTTCGAAGTATCATGCGGCGAGGCGCTTGAGAACCCCAAAATTAAGTCTCTCGGAC 586  
QY 730 TCGGAAGTCTCGAGGCGCTATGCGGCGCAAAAGCGGCGCCATTTGGCTGCGTAAAGGTT 789  
DB 585 TCGGAAGTCTCGAGGCGCTATGCGGCGCAAAAGCGGCGCCATTTGGCTGCGTAAAGGTT 526  
QY 790 AAGAACTACTGAATGAGTGTCTGAGATCTTCAGTGTCTGGCTCTTCTTCGCGATC 849  
DB 525 AAGAACTACTGAATGAGTGTCTGAGATCTTCAGTGTCTGGCTCTTCTTCGCGATC 466  
QY 850 GGCATGAGCGCGGCAAAATTCCTGGGCGGACAGCTTGAATTCGATTCAGATGTTAT 909  
DB 465 GGCATGAGCGCGGCAAAATTCCTGGGCGGACAGCTTGAATTCGATTCAGATGTTAT 406  
QY 910 GTGGAACCAAGCCAGGTTCCACTACACCAAGTGTAAAGGTTATTTGCTGTCGCGAC 969  
DB 405 GTGGAACCAAGCCAGGTTCCACTACACCAAGTGTAAAGGTTATTTGCTGTCGCGAC 346  
QY 970 GTGCGAGACAGAGTACCTGAGGCGATTCAGGCTGAGTACAGGCTGATGGTGTGA 1029  
DB 345 GTGCGAGACAGAGTACCTGAGGCGATTCAGGCTGAGTACAGGCTGATGGTGTGA 286  
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DB 285 TTGGAAGCTGAGCACTACCTGCGAGGAGATCGGTGCAAGAGGAAAGTCTGATGACTA 226  
QY 1090 TATTTAGGTGTAGCAACCAAGTACCTGCAATAGTACAGTGTGCTGGAAGCGCT 1149  
DB 225 TATTTAGGTGTAGCAACCAAGTACCTGCAATAGTACAGTGTGCTGGAAGCGCT 166  
QY 1150 CTCTGATGCGGTTTATGCGGTTGTCTAGTACGCTCAGATTTGAGATACCTGATGATT 1209  
DB 165 CTCTGATGCGGTTTATGCGGTTGTCTAGTACGCTCAGATTTGAGATACCTGATGATT 106  
QY 1210 TATGCTGCTTAGTACGATGCTATCTTATGTTAGGATCCAGAGTATGCTGAGCTCTG 1269  
DB 105 TATGCTGCTTAGTACGATGCTATCTTATGTTAGGATCCAGAGTATGCTGAGCTCTG 46  
QY 1270 AACTATTACTGGATACCTATTTCG 1293  
DB 45 AACTATTACTGGATACCTATTTCG 22

RESULT 4  
CC658769  
LOCUS  
DEFINITION  
CC658769 Zea mays genomic clone ZMMBMA056N04,  
genomic survey sequence.  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
CC658769 774 bp DNA linear GSS 19-JUN-2003  
OCWEP74TH\_ZM\_0.7\_1.5\_KB Zea mays genomic clone ZMMBMA056N04,  
genomic survey sequence.  
CC658769.1 GI:3202228  
GSS.  
Zea mays  
Zea mays  
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (bases 1 to 774)  
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,  
Citek, R.W., Nunberg, R.A., Robbins, D. and Lakey, N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Other GSSs: OGWEP74TV  
Contact: Cathy Whitelaw  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TR  
Class: sheared ends.  
Location/Qualifiers  
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ORIGIN

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QY 61 GCGAAGCCAAAGCCAACTGAGTAAGCAGCTATGAGGAGGATCCGCGCGCGCTCCGTCGCGC 120  
DB 146 GCGAAGCCAAAGCCAACTGAGTAAGCAGCTATGAGGAGGATCCGCGCGCGCTCCGTCGCGC 205  
QY 121 AGCGCATCTGCATCATATGAGAGCGGTCCGCTGGCACAAGGAGGATCTACCGCGCC 180  
DB 206 AGCGCATCTGCATCATATGAGAGCGGTCCGCTGGCACAAGGAGGATCTACCGCGCC 265  
QY 181 CGCGCGGAGCTCAAGCTGTGTCTTTCGAGGAGCTGGATGGCCAAAGACATCCGCGCGGCG 240  
DB 265 CGCGCGGAGCTCAAGCTGTGTCTTTCGAGGAGCTGGATGGCCAAAGACATCCGCGCGGCG 325  
QY 241 GGGCAGCTCACCAACCAACCGAGCTTCGAGAACTTCCCGGGCTTCCCAAGCGCATCATG 300  
DB 326 GGGCAGCTCACCAACCAACCGAGCTTCGAGAACTTCCCGGGCTTCCCAAGCGCATCATG 385  
QY 301 GGGCGGAGCTCATGAGCAACTGCGCGGAGTCCCTGCGCTTTGGCAACCAATCCTC 360  
DB 386 GGGCGGAGCTCATGAGCAACTGCGCGGAGTCCCTGCGCTTTGGCAACCAATCCTC 445  
QY 361 TCCGAGACCGCTCACCGCGCTCGACTTTTCGCGCTGCCCATTCGAGTTAGTGCAGATCC 420  
DB 446 TCCGAGACCGCTCACCGCGCTCGACTTTTCGCGCTGCCCATTCGAGTTAGTGCAGATCC 505  
QY 421 ACAACGCTCTCGCGATCGGTTATCGTTGCCAGGAGCGCTCGCGGCGCGCTCCAC 480  
DB 506 ACAACGCTCTCGCGATCGGTTATCGTTGCCAGGAGCGCTCGCGGCGCGCTCCAC 565  
QY 481 TTCCCGGGTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540  
DB 566 TTCCCGGGTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 625  
QY 541 GCGGCGGCGCTCTTCGTAAGCAAGCCATCGCGCTCATAGGCGGCGGCGG- ACTCCGCTAT 599  
DB 626 GCGGCGGCGCTCTTCGTAAGCAAGCCATCGCGCTCATAGGCGGCGGCGGAACTCCGCTAT 685  
QY 600 GGAGGAGTCCCAATTTCTCCACCAAGTACGCTGCCCAAGTCTACATCATCCACCGCGGCA 659

**RESULT 3**  
**EM351639**  
**LOCUS** 705 bp mRNA linear EST 16-JAN-2002  
**DEFINITION** MEST344-B12.73 ISUM5-RN Zea mays cDNA clone MEST344-B12 3', mRNA sequence.  
**ACCESSION** EM351639  
**VERSION** EM351639  
**KEYWORDS** EST.  
**SOURCE** Zea mays  
**ORGANISM** Zea mays  
**REFERENCE** Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
**AUTHORS** Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S.  
**TITLE** Expressed Sequence Tags from B73 Maize: various stages and tissues including seedlings treated with a variety of hormones  
**JOURNAL** Unpublished (2001)  
**COMMENT** Contact: Patrick S. Schnable  
 Schnable Laboratory  
 Iowa State University  
 G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA  
 Tel: 515-294-0975  
 Fax: 515-294-3299  
 Email: schnable@iastate.edu  
 Individual basecall and confidence value were assigned using the Phred software.  
 (<http://dseqts.washington.edu/ventures/collabtr/direct/index.htm>#brt). Overall sequence quality assessment and vector trimming were conducted using the Lucy software (<http://www.tigr.org/softlab/>). Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve as spacers.  
**PCR Primers**  
**FORWARD:** primer T7-1 (AA TAC GAC TCA CTA TAG)  
**BACKWARD:** primer T3 (ATT AAC CCT CAC TAA AG)  
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**Location/Qualifiers**  
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 /clone="MEST344-B12"  
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 /clone\_lib="ISUM5-RN"  
 /notes="Vector: pT73PAC; Site 1: EcoRI; Site 2: NotI;  
 Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG),  
 Mixed mature tissues (17, 21, 38, 69, 77 DAG), Kernels  
 (3, 5, 10, 15, 20, 25, 30, DAP), Adventitious roots (65  
 DAG), Tassel (3-39 cm, 53 and 56 DAG), Immature ear  
 (0.2-3.0 cm, 53, 56, 59 DAG), Husk (73 DAG), Silk,  
 unpollinated first ear, ear shank, etiolated seedlings,  
 callus, Cycloheximide-treated callus, Anaerobic treated  
 seedlings, NAA (α-Naphthalene acetic acid)-treated  
 seedlings, Kinetin-treated seedlings, ACPG  
 (1-aminocyclopropane-1-carboxylic acid)-treated seedlings,  
 Brassinolide-treated seedlings, ABA (Absciscic  
 acid)-treated seedlings, GA (Gibberellic acid)-treated  
 seedlings, JA (Jasmonic acid)-treated seedlings. ds-cDNA  
 molecules were generated as follows. First-strand cDNA was  
 prepared from oligo-dT selected mRNA by priming with a  
 NotI oligo-dT primer (5'  
 AACTGGAGATTCGGCGCGAGGAATTTTCTTTTCTTTT). The  
 resulting DNA:RNA hybrid was treated with RNase H and used  
 as a template for DNA PolI-catalyzed second strand  
 synthesis. After the addition of EcoRI adaptors, the  
 ds-cDNAs were digested with NotI and size-selected. The

maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

FEATURES  
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ORIGIN		Query Match	98.5%	Score 1316;	DB 11;	Length 1380;
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		Matches 1331;	Conservative 0;	Mismatches 5;	Indels 2;	Gaps 1;
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QY	61	GGGAGCCCAAGCCAACTGAGTAAGCAGCTATGGAGGATCGCGCGCTCGCTCGCG	120			
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QY	181	CGCGCGAGCTCAAGCTGCTCTTCGAGGCTGATGCGCAACGACATCGCGCGGCG	240			
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QY	241	GGCGAGCTCACACCAACCGAGCTCGAGAACTTCCCGGGCTTCCCGGCTTCCCGG	300			
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DB	333	GGCGGAGCTCATGAGCAACTGCGCGCGAGTCCCTGCGCTTGGGACCAACATCCTC	392			
QY	361	TCGAGACCGCTCACCGCGCTCGACTTTTCGCTCGCCCTTCGAGTTAGTGACACTCC	420			
DB	393	TCGAGACCGCTCACCGCGCTCGACTTTTCGCTCGCCCTTCGAGTTAGTGACACTCC	452			
QY	421	ACAACCGTCTCGCGATCGGTTATCGTTGCGACGGAGCGCTCGCGCGGCTTCCAC	480			
DB	453	ACAACCGTCTCGCGATCGGTTATCGTTGCGACGGAGCGCTCGCGCGGCTTCCAC	512			
QY	481	TTCCCGGGTTCGATCATGAGCAACCGGATCTCCGCTTCGCTGCTGTAACGCT	540			
DB	513	TTCCCGGGTTCGATCATGAGCAACCGGATCTCCGCTTCGCTGCTGTAACGCT	572			
QY	541	GGCGCGCCCATCTTCGCTAACAGCCCATCGCGTCAATAGGCGCGGCGACTCCGCTATG	600			
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DB	633	GAGGAGTCAATTTCTTCACCAAGTACGCTCCAGTCTCATCATCAACCGCGCAAT	692			
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QY	721	CTCTGGGACTCGAAGTTGCGAGGCTATGGCGGCGCAACCGCGCGCCCATGSGTCG	780			

DB	753	CTCTGGGACTCGAAGTTGTCGAGGCGCTATGGCGGCGCAACGGCGGCCCATTTGCTGGC	812
QY	781	GTAAAGGTTAAGAACCTACTGAAATGGTCTGAGTCTTCAGGTCTGCGGCTCTTC	840
DB	813	GTAAAGGTTAAGAACCTACTGAAATGGTCTGAGTCTTCAGGTCTGCGGCTCTTC	872
QY	841	TTGCGCATCGGCGATGAGCGCGGACCAAAATTCCTGGGCGGACAGCTTGAATCGATTCA	900
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DB	933	GATGTTATGTGGAAACCAAGCCAGGTTCCACTCACACAGTGTAAAGGGTGTATTTGCT	992
QY	961	GCTGGCGAGCTGCGAGGCAAGAGTACCGTCAGGCGCATTTCTGCGCTGGATCAGGTC	1020
DB	993	GCTGGCGAGCTGCGAGGCAAGAGTACCGTCAGGCGCATTTCTGCGCTGGATCAGGTC	1052
QY	1021	ATGGCTGCATTTGGACGCTGAGCACTTACCTGCGAGGAGATCGGTGCGACAGAGGAAAGTCT	1080
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QY	1081	GATTGACTATATTTAGTGTAGCAACAGCAATCCATCGAATAGTCAAGTTGCGTGTGCTG	1140
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QY	1141	AAAGCGGCTCTCTGATGCGCGTTTATGCGCATGCGGTTGTCTGATGCTCAAGTTGAGATAC	1200
DB	1173	AAAGCGGCTCTCTGATGCGCGTTTATGCGCATGCGGTTGTCTGATGCTCAAGTTGAGATAC	1232
QY	1201	CTGATGATTTATGCTGCTTAGTGTAGCAAGTCTTATTCGTTAGGATCAGAGTATGTC	1260
DB	1233	CTGATGATTTATGCTGCTTAGTGTAGCAAGTCTTATTCGTTAGGATCAGAGTATGTC	1292
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genomic survey sequence.  
ACCESSION  
CG300268  
VERSION  
CG300268.1 GI:34214482  
KEYWORDS  
GSS.  
SOURCE  
Zea mays  
ORGANISM  
Zea mays  
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
REFERENCE  
1 (bases 1 to 871)  
Whitelaw C.A., Quackenbush J., Van Aken S., Utterback T.,  
Resnick A., Fraser C.M., Budiman M.A., Bedell J.A., Rohlfing T.,  
Citek R.W., Nurnberg A., Robbins D. and Lakey N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Other GSSs: OG2AE91TH  
Contact: Cathy Whitelaw  
TIGR Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TP  
Class: sheared ends.  
FEATURES  
Location/Qualifiers  
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source

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 5, 2004, 19:52:33 ; Search time 4011.94 Seconds  
(without alignments)  
9944.292 Million cell updates/sec

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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: em\_estba:\*  
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7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_estl1:\*  
10: gb\_est2:\*  
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24: em\_gss\_pro:\*  
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26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	871	65.2	871	29	CG300268
3	684	51.2	705	12	BM351639
4	664.2	49.7	774	29	CC658769

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DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
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REFERENCES  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

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Zea mays  
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1 (bases 1 to 1380)  
Hainey, C.P., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.  
Maize Mapping Project/BuPont Consensus Sequences for Design of Overgo Probes  
Unpublished (2002)  
2 (bases 1 to 1380)  
Coe, E.H.  
Direct Submission  
Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA  
If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the

ALIGNMENTS

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DEFINITION	Zea mays	1380 bp	mRNA	linear	HTC 16-OCT-2002
ACCESSION	AY104846	1380 bp	mRNA	linear	HTC 16-OCT-2002
VERSION	AY104846.1	GI:21207924			
KEYWORDS	HTC				
SOURCE	Zea mays				
ORGANISM	Zea mays				
REFERENCES					
AUTHORS					
TITLE					
JOURNAL					
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AUTHORS					
TITLE					
JOURNAL					
COMMENT					

128	QY	TCTGATCATATCGGAGCGGTCCGCTCGCAACAACGAGCCATCTACGCGCGCGCGCGG	187
129	DB	TTTGATGCTGGAAATGGACAGCAGACACACGCGCGGATCTATGATCTTAGAGCGG	168
188	QY	AGCTCAAGCTGTGTCTCTTCGAGGCGTGGATGGCCAAACGACATCGCGCGCGCGG	247
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248	QY	TCACCAACACACGATCGGAACTTCGCGGCTTCGCCAAACGGCATCATAGCGCGCG	307
229	DB	TAAACAACAACCAACGATCGGAACTTCCTCGGCTTCCTGAAGGTATTTCTCGTATTG	288
308	QY	ACCTCATGGACAACCTCGCGCGCGCATCCCTCGCTTTGGCACCAACATCTCTCCGAGA	367
289	DB	ATAATCGTTGAGAAATTCAGAAACAATCGAGAGATTTGGAACATCGATCTTCACGGAAA	348
368	QY	CGGTCAACCGCGTGGACTTTTCGGCTGCCATTCGAGTTAGTCGACAGTCCCAACACG	427
349	DB	CTGTTAACAAAGTTGATTTCTCATGAAACCGTTTAAGCTATTCTACTGATTCGAGACTG	408
428	QY	TCTCGCCGATCGGTTATCGTTGCAACGAGACCGTGCAGCGGCGCTCCCATCTCCCG	487
409	DB	TTCTCGCTGATTCGTAAATCAATTTCTACTGGAGCTGTTGCTAAACGTCTTAGCTTCACTG	468
488	QY	GGTCCGATGCA-----TACTGGAAACGGGGCATCTCCGCTGTGCGCTCTGTG	535
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529	DB	ACGAGCTGCTCGATTTTGGATTAAGCCCTCTTGCTGTATTGGTGGTGGTATTCAG	588
596	QY	CTATGGAGAGTCCAAATTCCTCAACAAGTACGGCTCCCAAGTCTACATCATCCAGCC	655
589	DB	CTATGGAGGAAGCTAATTTCTGACTAAGTATGGATCTAAGGTATATAATATCCATAGAA	648
656	QY	GCAATACCTTCCTGCTTCCAAATCATGACGACGAGGCGCTTCAGAACCCCAAAATTA	715
649	DB	GGGATACGTTTAGGGCGTCTAAGATTATGACGACGAGACTATGCTTAACCCGAGATTG	708
716	QY	AGGTCTCTGGACTCGGAAGTTGTGAGGCTATGGCGCGCAACGCGCGGCCCATTCG	775
709	DB	AAATGATTTTGGAACTCTGGGTGGTGGAGCGGTATGGAGATGAAATATGACGTGTCTTG	768
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829	DB	TGTTCTTTGCTATTGGTCTATGAGCCAGCTACGAAGTTTTTGGATGGCGAGCTTGAGCTTG	888
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956	QY	TTGCTGTCGCGAGCTGCGAGGACAAGAATGACCGTCAGGCCATTTCTGCGCTGGATCAG	1015
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1016	QY	GGTGCATGGCTGATTTGGACCGCTGAGCACTTACCTGCGAGGAGATCGGTGCAAGAGGAA	1075
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1076	QY	AGTCTGATT	1084
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PR 14-JUN-1999; 99US-0139119P.  
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PR 18-JUN-1999; 99US-0139454P.  
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PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140821P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142928P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 20-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144632P.  
PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
PR 21-JUL-1999; 99US-0145086P.  
PR 22-JUL-1999; 99US-0145087P.  
PR 22-JUL-1999; 99US-0145088P.  
PR 22-JUL-1999; 99US-0145192P.  
PR 23-JUL-1999; 99US-0145145P.  
PR 23-JUL-1999; 99US-0145218P.  
PR 23-JUL-1999; 99US-0145224P.  
PR 26-JUL-1999; 99US-0145276P.  
PR 27-JUL-1999; 99US-0145911P.  
PR 27-JUL-1999; 99US-0145918P.  
PR 27-JUL-1999; 99US-0145919P.  
PR 28-JUL-1999; 99US-0145951P.  
PR 28-JUL-1999; 99US-0146386P.  
PR 02-AUG-1999; 99US-0146388P.  
PR 02-AUG-1999; 99US-0146389P.  
PR 03-AUG-1999; 99US-0147038P.  
PR 04-AUG-1999; 99US-0147204P.  
PR 04-AUG-1999; 99US-0147302P.  
PR 05-AUG-1999; 99US-0147192P.  
PR 05-AUG-1999; 99US-0147260P.  
PR 06-AUG-1999; 99US-0147303P.  
PR 06-AUG-1999; 99US-0147416P.

PR 09-AUG-1999; 99US-0147493P.  
PR 09-AUG-1999; 99US-0147935P.  
PR 10-AUG-1999; 99US-0148171P.  
PR 11-AUG-1999; 99US-0148319P.  
PR 12-AUG-1999; 99US-0148341P.  
PR 13-AUG-1999; 99US-0148565P.  
PR 13-AUG-1999; 99US-0148684P.  
PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149723P.  
PR 20-AUG-1999; 99US-0149929P.  
PR 23-AUG-1999; 99US-0149902P.  
PR 23-AUG-1999; 99US-0149930P.  
PR 25-AUG-1999; 99US-0150566P.  
PR 26-AUG-1999; 99US-0150884P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151065P.  
PR 27-AUG-1999; 99US-0151080P.  
PR 27-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154059P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
PR 05-OCT-1999; 99US-0157753P.  
PR 06-OCT-1999; 99US-0157865P.  
PR 07-OCT-1999; 99US-0158029P.  
PR 08-OCT-1999; 99US-0158232P.  
PR 12-OCT-1999; 99US-0158369P.  
PR 13-OCT-1999; 99US-0159293P.  
PR 13-OCT-1999; 99US-0159294P.  
PR 13-OCT-1999; 99US-0159295P.  
PR 14-OCT-1999; 99US-0159329P.  
PR 14-OCT-1999; 99US-0159330P.  
PR 14-OCT-1999; 99US-0159331P.  
PR 14-OCT-1999; 99US-0159637P.  
PR 14-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161992P.  
PR 28-OCT-1999; 99US-0161993P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 32.5%; Score 434.6; DB 3; Length 1313;  
Best Local Similarity 67.2%; Pred. No. 3.3e-89;  
Matches 651; Conservative 0; Mismatches 304; Indels 14; Gaps 2;





CC preferably from RA4W, RA5L, RA5M, RA5I, RA5P, RA5V, RA6T, RA6S,  
CC RA6Q, RA6S, and RA6N. The method is useful for reducing the toxicity of  
CC toxic proteins, reducing allergenicity of food and increasing the  
CC digestibility of food. The invention provides an efficient and low cost  
CC method as compared to prior art. The present sequence encodes a mutant A.  
CC thaliana TRR as an S-tagged/His-tagged fusion protein.

XX SQ Sequence 6357 BP; 1521 A; 1640 C; 1652 G; 1544 T; 0 U; 0 Other;

Query Match 32.6%; Score 435.8; DB 9; Length 6357;  
Best Local Similarity 65.9%; Pred. No. 2.6e-89;  
Matches 654; Conservative 0; Mismatches 327; Indels 12; Gaps 1;

Qy	108	CGCTCCGCTCCGCGCGCGAGCTCAACCTGTGCTTCTCGAGGCTGATGGCAACGA	167
Db	5345	CGAACTCAACAACAGGCTCTGTATCTAGTAGAGTGCCACGCGACACACGGCGC	5404
Qy	168	CATCTACGCGCGCGCGAGCTCAACCTGTGCTTCTCGAGGCTGATGGCAACGA	227
Db	5405	GATTTACGCGAGCTAGGCTGAATTAACCTCTCTCTCGAAGATGATGGCTAACGA	5464
Qy	228	CATCGCGCGCGCGAGCTCAACCTCAACCGAGCTCGAGACTTCCGGGCTTCCC	287
Db	5465	CATCGCTCCGCGGTCACTAACCAACCAACCGAGCTTCCCGGATTTCC	5524
Qy	288	CAACGCGATCATGGCGCGGACCTCATGGACAACTGCGCGCGAGTCCCTGCGTTGG	347
Db	5525	AGAGGTATTCGAGTAGAGTCACTGACAAATTCGTAACAAATCGGAGCAATCGG	5584
Qy	348	CACCAATCTCTCCGAGACGCTCACCGCGTGCATTTTCGGCTGCCATTCGAGT	407
Db	5595	TACTACGATATTACAGAGCGGTGACGAAATCGATTTCTTCGAAACCGTTAAGCT	5644
Qy	408	TAGTGCAGACTCCACACCGCTCTCGCGGATGCGGTATCTGTCACGGGAGCGTGC	467
Db	5645	ATTACAGATTCGAGGCAATTCGCTGACGCTGTGATTTCTGCTACTGAGCTGTGC	5704
Qy	468	CGCGCGCTCCACTTCCCGGCTCGATGCA-----TACTGGAACCGCGGAT	515
Db	5705	TAAGCGCTTAGCTCGTTGATCTGCTGTAAGGTTCTGCGAGTTTCTGGAACCGTGAAT	5764
Qy	516	CTCGCGCTGCTGCTGCGGTCGCGCCCATCTTCGTTACAGGCCATCGCGCT	575
Db	5765	CTCGCATGCGTGTTCGACGAGCTGCTCGATATTCGTAAACCTCTTCGCT	5824
Qy	576	CATAGCGCGCGGCTCCGCTATGAGGAGTCCAAATTCCTACCAAGTACGCTCCCA	635
Db	5825	GATGGTGGAGGCGATTACGAAATGGAAGACAACTTTCTTACAAATATGATCCAA	5884
Qy	636	CGTCTACATCATCCACGCGCAATCTTCGCTCTTCCAGATCATGCGGCGAGGCG	695
Db	5885	AGTGATATAATCCATCGCTAGATGCTTTAATCGCTTAAGATATGCGAGCGGCGC	5944
Qy	696	GCTTGAGAACCCCAAAATTAAGGTCTCTGCGACTCGGAAGTTGTGCGAGGCTATGCGG	755
Db	5945	TTTGTCTAATCTAAGATTGATGATTGGAATCGTCTGTGTGGAAGCTTATGAGA	6004
Qy	756	CGCAACGCGCGCCATCTGGCTGGCGTAAAGTTAAGACCTACTGAATGTGAGTCTC	815
Db	6005	TGGAGAAAGAGATGCTTGAGGAGTGAAGTGAAGATGTTTACCGGTGATGTTTC	6064
Qy	816	GGATCTTCAGGTGCTGCGCTCTTCTCGCCATCGGCGATGAGCGCGGACCAATTCCT	875
Db	6065	TGATTTAAAGTTTCTGGATTGTTTGTCTTGTCTATGCTCATGAGCCAGCTACCAAGTTT	6124
Qy	876	GGCGCGACAGCTTGAATCTGATTCAGTGTATGTGGAACCAACCGAGTTCACATCA	935
Db	6125	GGATGGTGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	6184
Qy	936	CACCAAGTGAAGGTGATTTGCTGCGGCGACGTCGAGGACCAAGATACCGTCAGCG	995
Db	6185	GACTAGCTTCCCGAGTTTTCGCTGCGGCTGATGTTTCAAGATAGAGATAGCGAGC	6244

Qy	996	CATTACTGCGCTGGATCAGGGTGCATGCTGCAATTCGAGCTACCTGCGAGGA	1055
Db	6245	CATCACTGCTGCGAGGAAGTGGTGCATGCGAGCTTTGGATGCGAGGATTTACAAGA	6304
Qy	1056	GATCGGTGCGACAGAGGGAAGTCTGATTCAT	1088
Db	6305	GATTGGATCTCAGCAAGGTAAGAGTGATTGAGT	6337

## RESULT 14

ADD26533  
ID ADD26533 standard; DNA; 6357 BP.

XX AC ADD26533;

XX DT 15-JAN-2004 (first entry)

XX DE Thalecress thioredoxin reductase RYN-I/S-tag/His-tag mutant DNA.

XX KW Thioredoxin reductase; TRR; cofactor specificity;  
XX KW computational mutagenesis; substrate specificity; PDA;  
XX KW protein design automation; toxic protein; food allergenicity;  
XX KW food digestibility; thalecress; ds; mutant; plant.

XX OS Synthetic.

XX OS Arabidopsis thaliana.

XX PN US2003100743-A1.

XX PD 29-MAY-2003.

XX PF 06-MAY-2002; 2002US-00141531.

XX PR 04-MAY-2001; 2001US-0289029P.

XX PR 05-APR-2002; 2002US-0370609P.

XX PR 29-APR-2002; 2002US-0376682P.

XX PA (DALM/) DALMIA B K.

XX PA (BRIG/) BRIGGS S P.

XX PA (VALG/) VAL G D.

XX PA (DESJ/) DESJARLAIS J R.

XX PA (HEIF/) HEIFETZ P.

XX PA (LUGI/) LUGINEUHL P.

XX PA (MUCH/) MUCHHAL U.

XX PI Dalmia BK, Briggs SP, Val GD, Desjarlais JR, Heifetz P;

XX PI Luginbuhl P, Muchhal U;

XX PI WPI; 2003-801212/75.

XX DR P-PSDB; ADD26549.

XX PT

XX PT

XX PT

XX PT

XX PT

XX PS

XX PS Disclosure; Fig 16; 125pp; English.

XX The invention relates to altering the cofactor specificity of thioredoxin  
XX reductase (TRR) comprising computational mutagenesis. Also included are  
XX altering the substrate specificity of TRR or cofactor specificity of a  
XX target protein, a variant TRR protein that reduces a protein that reduces  
XX a thioredoxin protein (obtained from an organism selected from  
XX Escherichia coli, Bacillus subtilis, Mycobacterium leprae, Saccharomyces,  
XX Neurospora crassa, Arabidopsis, and human), a variant TRR protein fused  
XX to a second protein (that is either a wild-type TRR protein, thioredoxin,  
XX or a variant TRR protein), producing a plant with a modified TRR protein,  
XX a transformed plant prepared by the method and a transformed seed of the  
XX transformed plant. The cofactor specificity of the variant TRR is altered  
XX such that the variant preferentially binds NADPH compared to NADH, or  
XX vice versa. The protein design cycle comprises protein design automation  
XX (PDA (RTM)). This design cycle comprises the sequence design algorithm,  
XX or a force field calculation. The variant TRR protein is fused to the



Matches 657; Conservative 0; Mismatches 324; Indels 12; Gaps 1;			
QY	108	CGCTCGCTCCGACGCGCATCTGCATCATCGGAGCGTCCGCTGCGCACACGCGGACG	167
Db	5345	CGAAACTCACAACACAGGCTCTGTATGTAGAGATGCGCCAGCGGCACACACGCGCGC	5404
QY	168	CATCTACGGCGCGCGCGAGCTCAAGCTGTCTTCGAGGGCTGATGGCCAAACGA	227
Db	5405	GAFTTACGAGTAGGCTGAATTAACCTTCTCTCGAAGATGATGGCTTAACGA	5464
QY	228	CATCGCGCGCGCGGAGCTCACACACACACGAGCTGAGAGATTCGCCGGCTTCC	287
Db	5465	CATCGCTCCGCTGTGCTCAACTAACACACACGAGCTGAGAGATTCGCCGGATTC	5524
QY	288	CAACGCGATCATGGCGCGAGCTCATGACACACTGCGCGCGAGCTCCGCTTTGG	347
Db	5525	AGAGGATATTCGAGTAGAGCTACTGACAAATTCGTAACATCGAGCGATTCGG	5584
QY	348	CACCAACATCTCTCCGAGACGCTCACCGCTCGACATTTTCGGCTCGCCATTCGAGT	407
Db	5585	TACTACGATATTACAGACGCGTACGAAAGTCTGATTTCTTCGAAACCGTTAAGCT	5644
QY	408	TAGTCAGACTCCACACCGTCTCGCGATCGGCTTATGTTGCGACGGAGCGCTGCG	467
Db	5645	ATTCAGAGATTCAGAGGCAATTCGCTGACGCTGTGATTCGCTACTGGAGCTGTGC	5704
QY	468	GGCGGCGCTCCACTTCCCGGCTCCGATGCA-----TACTGGAACCGCGGAT	515
Db	5705	TAAGCGGCTTACCTTCGTTGATCTGGTGAAGTTCTGGAGTTCTGGAACCGTGAAT	5764
QY	516	CTCCGCTGTGCGCTGTGACGCTGCGCGCGCATCTTCGTAACAGCCCATCGCGT	575
Db	5765	CTCCGCTGTGCGCTGTGACGCTGCGCGCGCATCTTCGTAACAGCCCATCGCGT	5824
QY	576	CATAGCGCGCGGAGCTCCGCTATGAGGAGTCCAAATTCCTCACCAAGTACGGCTCCA	635
Db	5825	GATCGTGAGCGGATTCAGCAATGGAAGACCAAACTTCTTACAAATATGATCCAA	5884
QY	636	CGTCTACATCATCCACCGCGCAATACCTTCGCTGCTTCCAGATCATGCGGCGGCG	695
Db	5885	AGTGATATATATCATCCGCGGAGTCTTTCGCTGCTTCAAGATATGACGCGGCG	5944
QY	696	GCTTGAGAACCCAAATTAAGTCTCTCGGACCTCGGAAGTTGTCGAGGCTATGGGG	755
Db	5945	TTTGCTAATCTTAAGATTTGATGATTTGGAATCTGCTGTGTGGAAGCTTATGGAGA	6004
QY	756	CGCAACCGCGCGCCCATTTGGCTGCGGTAAAGTTAAGAACTTACTCAATGGTGAAGTCTC	815
Db	6005	TGAGAGAAAGAGATGTCTTGGAGATTAAGATGGAATGTTTACCGGTGATGTTTC	6064
QY	816	GGATCTTCAAGTGTGCGCTCTTCTCCCATCGGCAATGAGCGGCGGACCAATTCCT	875
Db	6065	TGATTTAAAGTTTCTGGATTTGTTCTTGTCTATTTGTTCAAGCCAGCTTACCAAGTTT	6124
QY	876	GGCGGACAGCTTGAATCGATGCTTATGTGGAACCAAGCCAGGTTCCACTCA	935
Db	6125	GGATGGTGTGTTGATTAAGATTCGATGTTATGTTGTACAGAGCTGTGTTACTACACA	6184
QY	936	CACAGTGTAAAGGGTATTTGCTGCTGGGACGTGCGAGGACAGAAATACCGTCAGGC	995
Db	6185	GACTAGCTTCCGCGAGTTTTCCTCGCGGTGATGTTTCAGGATAGAGATAGGCAAGC	6244
QY	996	CATTACTGCGCTGAGTACAGGGTGCATGCTGATTTGGACGCTGACACTACTCGCAGA	1055
Db	6245	CATCACTGCTGCGAGAACCTGGGTGCGATGCGAGCTTTGGATGAGAGCATCTTACAGA	6304
QY	1056	GATCGGTGCACAGGAGGGAAGTCTGATTTGACT 1088	
Db	6305	GATTGGATCTCAGCAAGGTAAGAGTGTGAGT 6337	

RESULT 12  
AAL54493

AAL54493 standard; DNA; 6357 BP.  
AAL54493;  
10-APR-2003 (first entry)  
Thioredoxin reductase variant DNA sequence #15.  
Ophthalmological; virucide; vulnerary; vasotropic; antiallergic;  
cofactor specificity; thioredoxin reductase; TR; non-allergenic food;  
computational mutagenesis; scaffold protein; oil body; animal feed;  
digestibility; gluten; protein disulfide isomerase; PDI; enzyme;  
scleroprotein; galled; food; nitrosative stress response; eye disease;  
cataract; oxidative stress; ischemic-reperfusion; acute lung injury; ds.  
Unidentified.  
WO200290300-A2.  
14-NOV-2002.  
06-MAY-2002; 2002WO-US014358.  
04-MAY-2001; 2001US-0289023P.  
05-APR-2002; 2002US-0370609P.  
29-APR-2002; 2002US-00370609.  
(XENC-) XENCOR.  
(SYCN) SYNGENTA PARTICIPATIONS AG.  
Briggs SP, Dalmia BK, Del Val G, Desjarlais JR, Heifetz P;  
Luginbuhl P, Muchhal U;  
WPI; 2003-111951/10.  
Altering cofactor specificity of target protein, e.g. thioredoxin  
reductase, useful for reducing antigenicity of glutens in wheat, barley,  
or treating disulfide linkages present in proteins, by computational  
mutagenesis.  
Disclosure; Fig 16; 212pp; English.  
The invention relates to a novel method for altering the cofactor  
specificity of a target protein (e.g. thioredoxin reductase (TR)) by  
computational mutagenesis. This method involves inputting a set of  
coordinates for a scaffold protein comprising amino acid positions,  
applying at least one protein design cycle; and generating a set of  
candidate variant proteins with altered cofactor specificity. The novel  
method is useful for altering the cofactor specificity of TR scaffold  
proteins chosen from *Escherichia coli*, *Bacillus subtilis*, *Mycobacterium*  
*leprae*, *Saccharomyces*, *Neurospora crassa*, *Arabidopsis*, and human. Another  
method of the invention is useful for making oil bodies which are useful  
in the preparation of non-allergenic foods, or in the preparation of  
animal feeds to improve the digestibility of the feeds. The variant TR  
protein is useful for reducing the antigenicity of glutens in wheat, rye  
or barley, to reduce alternative substrates for thioredoxin reductases,  
including a number of plant and mammalian proteins found to contain  
thioredoxin domains e.g. protein disulfide isomerase (PDI). The variant  
TR protein is useful as a redox partner in compositions used for treating  
disulfide linkages present in proteins such as enzymes, e.g., proteases,  
amylases, etc; and structural proteins such as scleroproteins.  
Compositions comprising variant TR proteins and PDI are useful for  
generating protein disulfide crosslinks yielding high molecular weight or  
gelled compositions, and thus is useful in food processing. A further  
method of the invention is useful for producing plants expressing variant  
TR protein, e.g., corn and soybean provides grains with altered storage  
protein quality as well as grains that perform qualitatively differently  
from normal grain during industrial processing or animal digestion of  
variant TR proteins in combination with thioredoxin, which can be used to  
manipulate nitrosative stress, to upregulate nitrosative stress  
responses, and thus is useful for treating eye diseases, such as  
cataracts, where it inhibits or reverse formation of cataract in eye. The  
variant TR protein in combination with thioredoxin is also useful for